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SEARCH REQUEST FORM

11-771

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Art Unit: _____

10E03

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 12-1-98
Searcher: POB x8-4291
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Search Site

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Type of Search

1 N.A. Sequence
2 A.A. Sequence
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 WISE (TM)

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Msrch_p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 30 13:10:04 1998; MasPar time 14.06 Seconds

Tabular output not generated. 782.765 Million cell updates/sec

Title: >US-09-033-662-2
 Description: (1-221) from US09033662.pep
 Perfect Score: 221
 Sequence: 1 MRCRISGRPPAPGVPAQA.....COGRGLNDTCRCRLRR 221

Scoring table: TABLE uniprottable
 Gap 60

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
 Listing first 100 summaries

Database: spltembl6
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 3.343; Variance 0.421; Scale 7.933

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	149	67.4	207	4	VEGF RELATED FACTOR IS	0.00e+00
2	39	17.6	207	11	VASCULAR ENDOTHELIAL G	3.35e-92
3	26	11.8	116	11	VASCULAR ENDOTHELIAL G	6.91e-52
4	23	10.4	150	11	VASCULAR ENDOTHELIAL G	6.67e-43
5	10	4.5	148	13	VASCULAR ENDOTHELIAL G	3.03e-07
6	10	4.5	194	13	VASCULAR ENDOTHELIAL G	3.03e-07
7	8	3.6	532	4	SODIUM CHANNEL	8.91e-03
8	7	3.2	96	4	VASCULAR ENDOTHELIAL G	9.02e-01
9	7	3.2	106	4	NEUROGENIC LOCUS NOTCH	9.02e-01
10	7	3.2	189	5	ZK899.3	9.02e-01
11	7	3.2	193	5	CORE PROTEIN (FRAGMENT	9.02e-01
12	7	3.2	207	2	NITRILE HYDROLASE ALPH	9.02e-01
13	7	3.2	207	14	ORF36L	9.02e-01
14	7	3.2	221	14	HEXON-ASSOCIATED STRUC	9.02e-01
15	7	3.2	232	4	VASCULAR ENDOTHELIAL G	9.02e-01
16	7	3.2	276	2	PUTATIVE REPLICATION P	9.02e-01
17	7	3.2	305	10	LEUCINE RICH REPEAT-LI	9.02e-01
18	7	3.2	309	2	LYASE	9.02e-01
19	7	3.2	479	11	ABL3 BINDING PROTEIN	9.02e-01
20	7	3.2	489	2	AKLAVINONE C-11 HYDROX	9.02e-01

21	7	3.2	508	2	PLCC	9.02e-01
22	7	3.2	641	2	OUTER MEMBRANE PROTEIN	9.02e-01
23	7	3.2	691	2	HYPOTHETICAL 75.7 KD P	9.02e-01
24	7	3.2	757	4	SKELTAL MUSCLE ABUNDA	9.02e-01
25	7	3.2	901	10	HYPOTHETICAL 101.5 KD	9.02e-01
26	7	3.2	920	4	THYROID HORMONE RECEPT	9.02e-01
27	7	3.2	1149	4	51C PROTEIN	9.02e-01
28	7	3.2	1258	4	INOSITOL POLYPHOSPHATE	9.02e-01
29	7	3.2	1529	4	KIAA0304	9.02e-01
30	7	3.2	1851	5	HYPOTHETICAL PROTEIN C	9.02e-01
31	7	3.2	2108	2	POLYKETIDE SYNTHASE	9.02e-01
32	7	3.2	2160	5	ZC101.2D (FRAGMENT)	9.02e-01
33	7	3.2	2347	5	ZC101.2A (FRAGMENT)	9.02e-01
34	7	3.2	29	5	OMEGA-CONOTOXIN WVID	9.02e-01
35	6	2.7	68	14	REVERSE TRANSCRIPTASE	5.62e+01
36	6	2.7	75	6	VASCULAR ENDOTHELIAL G	5.62e+01
37	6	2.7	81	2	TRNA PSEUDOURIDINE SYN	5.62e+01
38	6	2.7	87	13	N1-HEART DEVELOPMENTAL	5.62e+01
39	6	2.7	103	2	ORF12	5.62e+01
40	6	2.7	106	2	CORE PROTEIN (FRAGMENT	5.62e+01
41	6	2.7	120	14	NEF PROTEIN (FRAGMENT)	5.62e+01
42	6	2.7	121	10	ACYL CARRIER PROTEIN	5.62e+01
43	6	2.7	125	14	GAG PROTEIN (FRAGMENT)	5.62e+01
44	6	2.7	125	14	GAG PROTEIN (FRAGMENT)	5.62e+01
45	6	2.7	133	2	HYPOTHETICAL 13.4 KD P	5.62e+01
46	6	2.7	151	14	MOVEMENT PROTEIN	5.62e+01
47	6	2.7	202	14	NEF PROTEIN	5.62e+01
48	6	2.7	204	11	CODD FOR BY C. ELEGAN	5.62e+01
49	6	2.7	204	11	TRAI	5.62e+01
50	6	2.7	206	14	NEF PROTEIN	5.62e+01
51	6	2.7	206	14	NEF GENE (STRAIN KU9)	5.62e+01
52	6	2.7	206	14	NEF GENE (STRAIN KU10)	5.62e+01
53	6	2.7	206	14	NEF GENE (STRAIN KU5)	5.62e+01
54	6	2.7	207	14	NEF PROTEIN	5.62e+01
55	6	2.7	209	14	NEF PROTEIN	5.62e+01
56	6	2.7	209	14	NEF PROTEIN	5.62e+01
57	6	2.7	209	11	POSTAGLANDIN D SYNTH	5.62e+01
58	6	2.7	229	14	MC099	5.62e+01
59	6	2.7	234	11	ARGININE SPECIFIC THIO	5.62e+01
60	6	2.7	234	11	PHOSPHOPROTEIN	5.62e+01
61	6	2.7	241	14	PHOSPHOPROTEIN (P)	5.62e+01
62	6	2.7	241	14	PHOSPHOPROTEIN (P)	5.62e+01
63	6	2.7	241	14	PHOSPHOPROTEIN (P)	5.62e+01
64	6	2.7	242	14	COAT PROTEIN	5.62e+01
65	6	2.7	254	2	HYPOTHETICAL 25.8 KD P	5.62e+01
66	6	2.7	272	14	POLYPROTEIN (FRAGMENTS	5.62e+01
67	6	2.7	312	14	SGG1	5.62e+01
68	6	2.7	326	5	SIMILAR TO CUTICULAR C	5.62e+01
69	6	2.7	327	5	SIMILAR TO CUTICULAR COL	5.62e+01
70	6	2.7	334	5	HYPOTHETICAL PROTEIN T	5.62e+01
71	6	2.7	339	2	PLASMIN GENES TRAI - T	5.62e+01
72	6	2.7	340	5	P56L2.5	5.62e+01
73	6	2.7	358	11	VASCULAR ENDOTHELIAL G	5.62e+01
74	6	2.7	398	5	RRM-TYPE RNA BINDING P	5.62e+01
75	6	2.7	412	5	3-KETO-ACYL-COA THIOA	5.62e+01
76	6	2.7	412	5	HERPES SIMPLEX VIRUS T	5.62e+01
77	6	2.7	442	14	I-FLICE ISOFORM 4	5.62e+01
78	6	2.7	451	14	NUCLEOSID PROTEIN	5.62e+01
79	6	2.7	473	5	T0810.3	5.62e+01
80	6	2.7	480	4	CASPER	5.62e+01
81	6	2.7	493	14	DNA HELICASE	5.62e+01
82	6	2.7	533	11	RETINAL PIGMENT EPITHE	5.62e+01
83	6	2.7	552	14	PP-D13	5.62e+01
84	6	2.7	573	14	CHITINASE	5.62e+01
85	6	2.7	584	2	GROUP II INTRON-CONTAI	5.62e+01
86	6	2.7	620	2	OXAIOACETATE DECARBOXY	5.62e+01
87	6	2.7	690	5	ZC247.2	5.62e+01
88	6	2.7	730	5	F32D1.10 PROTEIN	5.62e+01
89	6	2.7	738	5	CC4.1 (FRAGMENT)	5.62e+01
90	6	2.7	739	11	NAGLU (EC 3.2.1.50) (A	5.62e+01
91	6	2.7	744	5	BOWEL	5.62e+01
92	6	2.7	749	2	SENSORY TRANSDUCTION H	5.62e+01
93	6	2.7	1065	5	PSOA	5.62e+01

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94 6 2.7 1240 4 015030 KIA0314 (FRAGMENT). 5.62e+01
95 6 2.7 1420 2 052666 CORE PROTEIN. 5.62e+01
96 6 2.7 1486 4 014637 LAMININ ALPHA 3B CHAIN 5.62e+01
97 6 2.7 1849 4 014572 PAC CLONE 248015 FROM 5.62e+01
98 6 2.7 2864 14 069422 POLYPEPTIDE. 5.62e+01
99 6 2.7 3895 14 065464 POLYPEPTIDE. 5.62e+01
100 6 2.7 4957 4 014687 ALR. 5.62e+01

ALIGNMENTS
RESULT 1
ID 016528; PRELIMINARY; PRT; 207 AA.
AC 016528;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.
GN VRF OR VEGF-B.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,
RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L.,
RA HAYWARD N., WEBER G.;
RL GENOME RES. 6:122-129(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-FIBROSARCOMA HT-1080;
RX MEDLINE; 96197355.
RA OLOFSSON B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-FIBROSARCOMA HT-1080;
RX MEDLINE; 96197355.
RA OLOFSSON B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE BRAIN;
RX MEDLINE; 96183052.
RA TOWNSON S., LAGERCRANTZ J., GRIMMOND S., SILINS G., NORDENSKJOLD M.,
RA WEBER G., HAYWARD N.K.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 220:922-928(1996).
DR EMBL; U52820; G1488261; -
DR MGI; 106199; VRF.
DR PROSITE; PS00249; PDGF; 1.
DR PFAM; PF00341; PDGF.
SQ SEQUENCE 207 AA; 21914 MW; 4EB6C405 CRC32;

Query Match 17.6%; Score 39; DB 11; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.35e-92;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 66 KOLVPCVTVORCGCCPDGECVPTGQHOVRMOILMI 104
QY 65 KOLVPCVTVORCGCCPDGECVPTGQHOVRMOILMI 103

RESULT 3
ID 035485; PRELIMINARY; PRT; 116 AA.
AC 035485;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B 186 PRECURSOR (FRAGMENT).
OS RATIUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-PLACENTA;
RA MANDRIOTA S.J., PEPPER M.S.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF032925; G2641622; -
DR PROSITE; PS00249; PDGF; 1.
DR PFAM; PF00341; PDGF.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12743 MW; 1C6E2733 CRC32;

Query Match 11.8%; Score 26; DB 11; Length 116;
Best Local Similarity 100.0%; Pred. No. 6.91e-52;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 16 KOLVPCVTVORCGCCPDGECVPTGQHOVRMOILMI 41
QY 65 KOLVPCVTVORCGCCPDGECVPTGQHOVRMOILMI 90
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RESULT 4
ID 054881: PRELIMINARY: PRT: 150 AA.
AC 054881:
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B (FRAGMENT).
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
CC EUTHERIA: RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA WEIL J., ESCHENHAGEN T., MITTMANN C., SCHOLZ H.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF022952; G2766602; -.
DR PROSITE: PS00249; PDGF; 1.
FT NON_TER 1 150
SQ SEQUENCE 150 AA; 17243 MW; D088D4D3 CRC32;

Query Match 10.4%; Score 23; DB 11; Length 150;
Best Local Similarity 100.0%; Pred. No. 6.67e-43;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 38 VPSCTVORCGGCCPDGECVP 60
QY 68 VPSCTVORCGGCCPDGECVP 90

RESULT 5
ID 042571: PRELIMINARY: PRT: 148 AA.
AC 042571:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 122.
GN VEGF.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: AMPHIBIA: ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RA CLEVERER O., TONISSEN K.F., SAHA M.S., KRIEG P.A.;
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF008593; G2271033; -.
DR PROSITE: PS00249; PDGF; 1.
DR PFAM: PF00341; PDGF.
SQ SEQUENCE 148 AA; 17234 MW; 83E936CE CRC32;

Query Match 4.5%; Score 10; DB 13; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.03e-07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 125 HSQCECRPK 134
QY 118 HSQCECRPK 127

RESULT 6
ID 042572: PRELIMINARY: PRT: 194 AA.
AC 042572:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 196.
GN VEGF.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: AMPHIBIA: ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RA CLEVERER O., TONISSEN K.F., SAHA M.S., KRIEG P.A.;
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
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DR EMBL: AF008594; G2271035; -.
DR PROSITE: PS00249; PDGF; 1.
DR PFAM: PF00341; PDGF.
SQ SEQUENCE 194 AA; 22672 MW; 74B8253A CRC32;

Query Match 4.5%; Score 10; DB 13; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.03e-07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 125 HSQCECRPK 134
QY 118 HSQCECRPK 127

RESULT 7
ID 060263: PRELIMINARY: PRT: 532 AA.
AC 060263:
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE SODIUM CHANNEL.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
CC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA ISHIBASHI K., MARUMO F.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 245:589-593(1998).
DR EMBL: AB010575; D1026837; -.
KW IONIC CHANNEL.
SQ SEQUENCE 532 AA; 59154 MW; 115D0C62 CRC32;

Query Match 3.6%; Score 8; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.91e-03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 130 GRPAPPG 137
QY 8 GRPAPPG 15

RESULT 8
ID 060720: PRELIMINARY: PRT: 96 AA.
AC 060720:
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 183 (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
CC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA JINGJING L., ROQUE R.S.;
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF062645; G3139081; -.
FT NON_TER 1 1
SQ SEQUENCE 96 AA; 11314 MW; D21D2474 CRC32;

Query Match 3.2%; Score 7; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 15 CECRPRK 21
QY 121 CECRPRK 127

RESULT 9
ID 014962: PRELIMINARY: PRT: 106 AA.
AC 014962:
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DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
DE NEUROGENIC LOCUS NOTCH 3 PROTEIN (FRAGMENT).
GN NOTCH3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERETIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95213014.
RA LARSSON C., LARDELLI M., WHITE I., LENDAHN U.;
RL GENOMICS 24:253-258(1994).
CC -1- FUNCTION: NOTCH 1, 2 AND 3 PLAY A COMBINATIONAL ROLE DURING
CC VARIOUS CELL FATE DECISIONS AND MORPHOLOGICAL MOVEMENTS IN THE
CC DEVELOPING CNS AND PROBABLY OTHER REGIONS OF THE EMBRYO.
CC -1- SIMILARITY: TO OTHER NOTCH-TYPE PROTEINS.
DR EMBL: X79439: 6763116; -.
KW DIFFERENTIATION; NEUROGENESIS; REPEAT; EGF-LIKE DOMAIN; TRANSMEMBRANE.
FT NON_TER 1 1
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11071 MW; B403D011 CRC32;

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 106;
Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 72 RPOPRSV 78
OY 143 RPOPRSV 149

RESULT 10
ID 023663 PRELIMINARY; PRT; 189 AA.
AC 023663;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ZK899.3.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RX KERSHAW J.;
RL SUBMITTED (SEP-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
RA BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAYTON M.,
RA DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
RA HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
RA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
RA RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SHALDON N., SMITH A.,
RA SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,
RA VAUDIN M., VAOGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
RA WILKINSON-SPROAT J., WOHLDMAN P.;
RA NATURE 368:32-38(1994).
RL NATURE 368:32-38(1994).
DR EMBL: Z37140: E257675; -.
SQ SEQUENCE 189 AA; 21101 MW; 0AB35BDE CRC32;

Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 189;
Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 80 VPLTEL 86
OY 53 VPLTEL 59

RESULT 11
ID 052677 PRELIMINARY; PRT; 193 AA.
AC 052677;

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DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE CORE PROTEIN (FRAGMENT).
GN ESCHERICHIA COLI.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-EC45;
RA WANG Y.-D., ZHAO S., HILL C.W.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF044505: G2921769; -.
FT NON_TER 1 1
FT NON_TER 193 193
SQ SEQUENCE 193 AA; 21272 MW; 9DB5CDD8 CRC32;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 193;
Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 155 PAPPGVP 161
OY 11 PAPPGVP 17

RESULT 12
ID 052737 PRELIMINARY; PRT; 207 AA.
AC 052737;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE NITRILE HYDRATASE ALPHA SUBUNIT.
OS RHODOCOCUS ERITHROPOLIS.
OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIIFORM.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-JCM6823;
RA MEDLINE: 93379358.
RA ROBERT D., NISHITAMA M., HORINOCHI S., BEPPU T.;
RA BIOSCI. BIOTECHNOL. BIOCHEM. 57:1323-1328(1993).
DR EMBL: D14454: G559379; -.
SQ SEQUENCE 207 AA; 23116 MW; C62357D4 CRC32;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 207;
Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 14 PAOPAVS 20
OY 17 PAOPAVS 23

RESULT 13
ID 039628 PRELIMINARY; PRT; 207 AA.
AC 039628;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ORF36L.
OS CYDIA POMONELLA GRANULOVIRUS.
OC VIRUSES; DSDNA VIRUSES. NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA JERLE J.A., VAN DER LINDEN I.F.A., VLAK J.M.;
RL VIRUS RES. 0:0-0(1997).
DR EMBL: AF002732: G23232189; -.
SQ SEQUENCE 207 AA; 23915 MW; D2F0E988 CRC32;

Query Match
Best Local Similarity 100.0%; Score 7; DB 14; Length 207;
Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 134 EVVPELT 140

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QY 50 EVVVPPLT 56

RESULT 14
ID 071198 PRELIMINARY; PRT; 221 AA.
AC 071198;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HEXON-ASSOCIATED STRUCTURAL PROTEIN PVIII PRECURSOR.
OS BOVINE ADENOVIRUS TYPE 1.
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; ADENOVIRIDAE; MASTADENOVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-10;
RA EVANS P.S., BENKO M., HARRACH B., LETCHWORTH G.J.;
RL VIROLOGY 244:173-185(1998).
DR EMBL; AF038868; G3135468; -.
SQ SEQUENCE 221 AA; 24149 MW; 22C990DC CRC32;

Query Match 3.2%; Score 7; DB 14; Length 221;
Best Local Similarity 100.0%; Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 124 GRGLELN 130
QY 204 GRGLELN 210






RESULT 15
ID 016889 PRELIMINARY; PRT; 232 AA.
AC 016889;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92168017.
RA HOUCK K.A., FERRARA N., WINER J., CACHIANES G., LI B., LEUNG D.W.;
RL MOL. ENDOCRINOL. 5:1806-1814(1991).
DR EMBL; S85192; G246156; -.
DR EMBL; S85224; E91787; -.
DR EMBL; S85199; E91787; JOINED.
DR EMBL; S85201; E91787; JOINED.
DR EMBL; S85219; E91787; JOINED.
DR EMBL; S85223; E91787; JOINED.
DR PROSITE; PS00249; PDGF; 1.
DR PRAM; PF00341; PDGF; 1.
SQ SEQUENCE 232 AA; 27042 MW; 344182D1 CRC32;

Query Match 3.2%; Score 7; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.02e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 GLECVPT 97
QY 85 GLECVPT 91

Search completed: Mon Nov 30 13:11:02 1998
Job time : 58 secs.

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97 6 2.7 1115 1 NCAL_MOUSE NEURAL CELL ADHESION M 2.50e+01
 98 6 2.7 1150 1 ZACA_HUMAN PROTEIN PHOSPHATASE PP 2.50e+01
 99 6 2.7 1188 1 DPOL_ADE40 DNA POLYMERASE (EC 2.7 2.50e+01
 100 6 2.7 3164 1 TEGU_HSV1 LARGE TEGUMENT PROTEIN 2.50e+01

ALIGNMENTS

RESULT 1
 ID VEGF_HUMAN STANDARD; PRT; 188 AA.
 AC P49765;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
 DE FACTOR).
 GN VEGF OR VRF.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96197355.
 RA OLOFSSON B., PAJUSOLA K., KAIPIAINEN A., VON EULER G., JOUKOV V.,
 RA SAKSELA O., ORPANA A., PETERSSON R.F., ALITALO K., ERIKSSON U.,
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., THOMSON S.,
 RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M.,
 RL WARD L., HAYWARD N., WEBER G.,
 RL GENOME RES. 6:122-129(1996).
 CC -1- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
 CC WITH VEGF.
 CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
 CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
 CC HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL; U48800; G1234825; -
 DR EMBL; U43369; G1216398; -
 DR MIM; 601398; -
 DR PROSITE; PS00249; PDGF; 1.
 KM MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
 SQ SEQUENCE 188 AA; 21261 MW; 35EA8904 CRC32;
 Query Match 53.8%; Score 119; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 PAQAPVSPDAPGHRKRVSMIDVTRATTCOPREYVVLVEIMGTAKOLVPSCTVQR 77
 Qy 17 PAQAPVSPDAPGHRKRVSMIDVTRATTCOPREYVVLVEIMGTAKOLVPSCTVQR 76
 Db 78 CGGCCPDGDLGECVPTGQHVYRQIMIRYPSOLGEMSLHSESCCECPKPKKSDAVRPD 136
 Qy 77 CGGCCPDGDLGECVPTGQHVYRQIMIRYPSOLGEMSLHSESCCECPKPKKSDAVRPD 135
 RESULT 2
 ID VEGF_MOUSE STANDARD; PRT; 188 AA.
 AC P49766;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
 DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
 GN VEGF OR VRF.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96197355.
 RA OLOFSSON B., PAJUSOLA K., KAIPIAINEN A., VON EULER G., JOUKOV V.,
 RA SAKSELA O., ORPANA A., PETERSSON R.F., ALITALO K., ERIKSSON U.,
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96183052.
 RA THOMSON S., LAGERCRANTZ J., GRIMMOND S., SILINS G.,
 RA NORDENSKJOLD M., WEBER G., HAYWARD N.K.,
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 220:922-928(1996).
 CC -1- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
 CC WITH VEGF.
 CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
 CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
 CC AND SKELETAL MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL; U48800; G1234825; -
 DR EMBL; U43837; G1314336; -
 DR MGD; MGI:106199; VRF.
 DR PROSITE; PS00249; PDGF; 1.
 KM MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
 SQ SEQUENCE 188 AA; 21442 MW; 7999A3C8 CRC32;
 Query Match 17.6%; Score 39; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 4.34e-99;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 66 KOLVPSCTVYRGGCGCPDGLGECVPTGQHVYRQIMIRI 104
 Qy 65 KOLVPSCTVYRGGCGCPDGLGECVPTGQHVYRQIMIRI 103
 RESULT 3
 ID VEGF_SHEEP STANDARD; PRT; 146 AA.
 AC P50412;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
 DE PERMEABILITY FACTOR) (VPF).
 GN VEGF.
 OS OVIS ARIES (SHEEP).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97117958.
 RA REDMER D.A., DAI Y., LI J., CHARNOCK-JONES D.S., SMITH S.K.,
 RA REYNOLDS L.P., MOOR R.M.,
 RL J. REPROD. FERTIL. 108:157-165(1996).
 CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS AND ENDOTHELIAL
 CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
 CC PERMEABILITY.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
 CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL; X89506; G899351; -
 DR PROSITE; PS00249; PDGF; 1.
 KM MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 26 BY SIMILARITY.
 FT CHAIN 27 146 VASCULAR ENDOTHELIAL GROWTH FACTOR.

BEST AVAILABLE

FT DISULFID 51 93 BY SIMILARITY.
 FT DISULFID 82 127 BY SIMILARITY.
 FT DISULFID 86 129 BY SIMILARITY.
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 100 100 POTENTIAL.
 SQ SEQUENCE 146 AA; 17247 MW; 4EBB20AE CRC32;

Query Match 3.2%: Score 7; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 127 CECRPRK 133
 121 CECRPRK 127

RESULT 4
 ID VEGF_GAVPO STANDARD; PRT; 164 AA.
 AC P26617;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPE).
 GN VEGF.
 OS CAVIA PORCELLUS (GUINEA PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BERSER B.;
 RL SUBMITTED (XXX-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL: M84230; G191307; -;
 DR PROSITE: PS00249; PDGF: 1.
 KW MITOGEN; GROWTH FACTOR; GLYCOPROTEIN.
 FT DISULFID 25 67 BY SIMILARITY.
 FT DISULFID 56 101 BY SIMILARITY.
 FT DISULFID 60 103 BY SIMILARITY.
 FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 59 59 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 74 74 POTENTIAL.
 SQ SEQUENCE 164 AA; 19330 MW; AEBBD3 CRC32;

Query Match 3.2%: Score 7; DB 1; Length 164;
 Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 CECRPRK 107
 121 CECRPRK 127

RESULT 5
 ID VEGF_PIG STANDARD; PRT; 190 AA.
 AC P49151;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPE).
 GN VEGF.
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.

RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE-HEART;
 RX MEDLINE: 95143284.
 RA SHARMA H.S., TANG Z.H., GHO B.C.H., VERDOUW P.D.;
 RL BIOCHIM. BIOPHYS. ACTA 1260:235-238(1995).
 CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL: X81380; G587560; -;
 DR PROSITE: PS00249; PDGF: 1.
 KW MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR.
 FT DISULFID 51 93 BY SIMILARITY.
 FT DISULFID 82 127 BY SIMILARITY.
 FT DISULFID 86 129 BY SIMILARITY.
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 100 100 POTENTIAL.
 SQ SEQUENCE 190 AA; 22368 MW; BA8CC907 CRC32;

Query Match 3.2%: Score 7; DB 1; Length 190;
 Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 90 GLECEPT 96
 85 GLECEPT 91

RESULT 6
 ID VEGF_BOVIN STANDARD; PRT; 190 AA.
 AC P15691;
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPE).
 GN VEGF.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
 RX MEDLINE: 90069608.
 RA LEUNG D.W., CACHINES G., KUANG W.-J., GOEDEL D.V., FERRARA N.;
 RL SCIENCE 246:1306-1309(1989).
 RN [2]
 RP SEQUENCE OF 27-190 FROM N.A.
 RX MEDLINE: 90121225.
 RA TISCHER E., GOSPODAROWICZ D., MITCHELL R., SILVA M., SCHILLING J.,
 RA LAU K., CRISP T., FIDDES J.C., ABRAHAM J.A.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 165:1198-1206(1989).
 RN [3]
 RP SEQUENCE OF 27-31.
 RX MEDLINE: 89286596.
 RA FERRARA N., HENZEL W.J.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 161:851-858(1989).
 CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL: M32976; G163007; -;

DR EMBL; M31836; G163809; -;
 DR EMBL; M33750; G163811; -;
 DR PIR; A33255; A33255.
 DR PIR; A33787; A33787.
 DR PIR; B40080; B40080.
 DR PROSITE; PS00249; PDGF; 1.
 DR MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; ALTERNATIVE SPLICING; SIGNAL.
 KW SIGNAL
 FT CHAIN 1 26
 FT SIGNAL 1 26
 FT DISULFID 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR.
 FT DISULFID 51 93 BY SIMILARITY.
 FT DISULFID 82 127 BY SIMILARITY.
 FT DISULFID 86 129 BY SIMILARITY.
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 100 100 POTENTIAL.
 FT VASPLIC 139 183 MISSING (IN BETA-FORM).
 FT VASPLIC 184 184 R -> K (IN BETA-FORM).
 SO SEQUENCE 190 AA; 22310 MW; E22F67ED CRC32;
 Query Match 3.2%; Score 7; DB 1; Length 190;
 Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 127 CECRPRK 133
 Qy 121 CECRPRK 127
 RESULT 7
 ID VEGF RAT STANDARD; PRT: 190 AA.
 AC P16612
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF).
 DE VEGF.
 GN VEGF.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-190.
 RX MEDLINE; 90207249.
 RA CONN G., BAYNE M.L., SODERMAN D.D., KWOK P.W., SULLIVAN K.A.,
 RA PALISI T.M., HOPE D.A., THOMAS K.A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:2628-2633(1990).
 CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PITUITARY, IN BRAIN, IN PARTICULAR IN SUPRACORTIC AND PARAVENTRICULAR NUCLEI AND THE CHOROID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTHEUM OF THE OVARY AND IN KIDNEY GLOMERULI.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL; M32167; G204288; -;
 DR PIR; A35987; A35987.
 DR PROSITE; PS00249; PDGF; 1.
 DR MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
 KW SIGNAL
 FT CHAIN 1 26
 FT SIGNAL 1 26
 FT DISULFID 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR.
 FT DISULFID 51 93 BY SIMILARITY.
 FT DISULFID 82 127 BY SIMILARITY.
 FT DISULFID 86 129 BY SIMILARITY.
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 100 100
 SO SEQUENCE 190 AA; 22396 MW; B64CA99F CRC32;
 Query Match 3.2%; Score 7; DB 1; Length 190;

Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 127 CECRPRK 133
 Qy 121 CECRPRK 127
 RESULT 8
 ID CR2_HORVU STANDARD; PRT: 202 AA.
 AC P23252;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DE COLD-REGULATED PROTEIN 2 (FRAGMENT).
 OS HORDEUM VULGARE (BARLEY).
 CC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE;
 CC CYPERALES; GRAMINEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. GEORGIE;
 RA CATTIVELLI L., BARTELS D.;
 RL PLANT PHYSIOL. 93:1504-1510(1990).
 CC -1- CONTAINS SEVERAL ARGININE RESIDUES IN CLOSE PROXIMITY WHICH MAY BE INVOLVED IN PROTEIN RNA INTERACTIONS.
 DR EMBL; M60733; G167028; ALT_INIT.
 DR PIR; B45512; B45512.
 FT NON_TER 1 1
 FT DOMAIN 116 125 ARG-RICH.
 SO SEQUENCE 202 AA; 21753 MW; BC9A9416 CRC32;
 Query Match 3.2%; Score 7; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 116 RCRCRR 122
 Qy 191 RCRCRR 197
 RESULT 9
 ID NHAA_PHOER STANDARD; PRT: 206 AA.
 AC P13446;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NITRILE HYDROLASE SUBUNIT ALPHA (EC 4.2.1.84) (NITRILASE) (NHASE).
 GN NHAA.
 OS RHODOCOCCUS ERITHROPOLIS.
 CC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIOFORM.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-N-774;
 RX MEDLINE; 89276338.
 RA Ikehara O., Nishiyama M., Horinouchi S., Beppu T.;
 RL EUR. J. BIOCHEM. 181:563-570(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N-774;
 RX MEDLINE; 91159474.
 RA HASHIMOTO Y., NISHIYAMA M., Ikehara O., Horinouchi S., Beppu T.;
 RL BIOCHIM. BIOPHYS. ACTA 1088:225-233(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ACV2;
 RA BIGEY F., CHEBBROU H., ARNAUD A., GALZY P.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE OF 1-187 FROM N.A.
 RC STRAIN-BREVIBACTERIUM SP. / STRAIN R312;
 RX MEDLINE; 91072222.
 RA MAYAUD J.-F., CERBELAUD E., SOUBRIER F., FAUCHER D., PETRE D.;
 RL J. BACTERIOL. 172:6764-6773(1990).

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RN [5]
RP SEQUENCE OF 1-19.
RC STRAIN-N-774.
RX MEDLINE: 89153549.
RA ENDO T., MATANABE I.;
RL FEBS LETT. 243:61-64(1989).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS).
RC STRAIN-R112.
RX MEDLINE: 97341231.
RA HUANG W., JIA J., CUMMINGS J., NELSON M., SCHNEIDER G., LINDQUIST Y.;
RL STRUCTURE 5:691-699(1997).
CC -1- FUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE
CC COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF
CC ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.
CC -1- CATALYTIC ACTIVITY: AN ALIPHATIC AMIDE -> A NITRILE + H(2)O.
CC -1- COFACTOR: BINDS A NON-HEME IRON.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: TO OTHER NITRILE HYDRATASES SUBUNIT ALPHA.
DR EMBL: X14668; G46430; -.
DR EMBL: X54074; G46412; -.
DR EMBL: 248769; G769825; -.
DR EMBL: M60264; G144092; -.
DR PIR: S04472; S04472.
DR PIR: B37806; B37806.
DR PDB: 1AHJ; 08-APR-98.
DR LYSASE; IRON; 3D-STRUCTURE.
FT INIT MET 0 0
FT METAL 109 109 IRON.
FT METAL 112 112 IRON.
FT METAL 113 113 IRON.
FT METAL 114 114 IRON.
FT METAL 117 117 P -> A (IN REF. 1).
FT CONFLICT 19 19 S -> T (IN REF. 4).
FT CONFLICT 19 19
SQ SEQUENCE 206 AA; 22865 MW; 41606C46 CRC32;

Query Match 3.2%; Score 7; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 3.30e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 PAQAPVS 19
QY 17 PAQAPVS 23

RESULT 10
ID VEGF_MOUSE STANDARD; PRT; 214 AA.
AC 000731;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92274860.
RA BREIER G., ALBRECHT U., STERRER S., RISAU W.;
RL DEVELOPMENT 114:521-532(1992).
RN [2]
RP SEQUENCE FROM N.A. (VEGF-1).
RX MEDLINE: 92355563.
RA CLAFFEY K.P., WILKINSON W.O., SPIEGELMAN B.M.;
RL J. BIOL. CHEM. 267:16317-16322(1992).
RN [3]
RP SEQUENCE OF 1-3 FROM N.A.
RX MEDLINE: 96216498.
RA SHIMA D.T., KUROKI M., DEUTSCH U., NG Y., ADAMIS A.P., D'AMORE P.A.;
RL J. BIOL. CHEM. 271:3877-3883(1996).
RN [4]
RP -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL

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CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: VEGF-1 AND VEGF-2 ARE SECRETED WHILST
CC VEGF-3 REMAINS CELL-SURFACE ASSOCIATED UNLESS RELEASED BY
CC HEPARIN.
CC -1- TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED MAINLY IN
CC THE CHOROID PLEXUS, PARAVENTRICULAR NEUROEPITHELIUM, PLACENTA AND
CC KIDNEY GLOMERULI. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADRENAL
CC GLAND AND IN SEMINIFEROUS TUBULES OF TESTIS. HIGH EXPRESSION OF
CC VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS.
CC -1- ALTERNATIVE PRODUCTS: THREE FORMS (VEGF-1, VEGF-2 AND VEGF-3) ARE
CC PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. 1st.
CC LONEST FORM (VEGF-3, SHOWN HERE) CONTAINS A BASIC INSERT LINKED
CC TO CELL-ASSOCIATION/HEPARIN-BINDING.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR EMBL: S37052; G249857; -.
DR EMBL: S38083; G249859; -.
DR EMBL: S38100; G249861; -.
DR EMBL: M95200; G202351; -.
DR EMBL: U41383; E215501; -.
DR PIR: A43351; A43351.
DR MGD: MGT-103178; VEGF.
DR PROSITE: PS00249; PDGF; 1.
DR MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; ALTERNATIVE SPLICING; SIGNAL.
KW SIGNAL.
FT CHAIN 1 26
FT DISULFID 27 24
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 85 85 INTERCHAIN (BY SIMILARITY).
FT VARSPLIC 100 100 PROBABLE.
FT VARSPLIC 140 140 K -> N (IN VEGF-1).
FT VARSPLIC 141 164 MISSING (IN VEGF-2).
FT VARSPLIC 141 208 MISSING (IN VEGF-2).
FT CONFLICT 117 118 GE -> ER (IN REF. 2).
SQ SEQUENCE 214 AA; 25283 MW; 403318AF CRC32;

Query Match 3.2%; Score 7; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.30e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 127 CECRPRK 133
QY 121 CECRPRK 127

RESULT 11
ID VEGF_HUMAN STANDARD; PRT; 215 AA.
AC P15692;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF OR VEGFA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90069608.
RA LEUNG D.W., CACHIANES G., KUANG W.-J., GOEDEL D.V., FERRARA N.;
RL SCIENCE 246:1306-1309(1989).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE: 90069609.
RA RECK P.J., HAUSER S.D., KRIYI G., SANJO K., WARREN T., FEDER J.;
RL CONNOLLY D.T.;
RL SCIENCE 246:1309-1312(1989).
RN [3]
RP SEQUENCE FROM N.A.

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RX MEDLINE: 91268072.
 RA TISCHER E., MITCHELL R., HARTMAN T., SILVA M., GOSPODAROWICZ D.,
 RA FIDES J.C., ABRAHAM J.A.;
 RL J. BIOL. CHEM. 266:11947-11954(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 92231879.
 RX WEINDEL K., MARME D., WEICH H.A.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 183:1167-1174(1992).
 RN [5]
 RP PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
 RX MEDLINE: 90062112.
 RA CONNOLLY D.T., OLANDER J.V., HEUVELMAN D., NELSON R., MONSELL R.,
 RA SIEBEL N., HAYMORE B.L., LEIMGRUBER R., FEDER J.;
 RL J. BIOL. CHEM. 264:20017-20024(1989).
 RN [6]
 RP SEQUENCE OF 27-41.
 RX MEDLINE: 93145946.
 RA FIEBICH B.L., JAEGER B., SCHOELLMANN C., WEINDEL K., WILTING J.,
 RA KOCHS G., MARME D., HUG H., WEICH H.A.;
 RL EUR. J. BIOCHEM. 211:19-26(1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
 RX MEDLINE: 97352774.
 RA MULLER Y.A., LI B., CHRISTINGER H.W., WELLS J.A., CUNNINGHAM B.C.,
 RA DE VOS A.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 94:7192-7197(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
 RX MEDLINE: 98035455.
 RA MULLER Y.A., CHRISTINGER H.W., KEYS B.A., DE VOS A.M.;
 RL STRUCTURE 5:1325-1338(1997).
 RN [9]
 RP STRUCTURE BY NMR OF 34-135.
 RX MEDLINE: 97477915.
 RA FARBRÖTHER W.J., CHAMPE M.A., CHRISTINGER H.W., KEYS B.A.,
 RA STROVANSKI M.A.;
 RL PROTEIN SCI. 6:2250-2260(1997).
 RN [10]
 RP STRUCTURE BY NMR OF 137-215.
 RX MEDLINE: 98298440.
 RA FARBRÖTHER W.J., CHAMPE M.A., CHRISTINGER H.W., KEYS B.A.,
 RA STROVANSKI M.A.;
 RL STRUCTURE 6:637-648(1998).
 CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
 CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
 CC PERMEABILITY.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS OF VEGF ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE (VEGF-121, VEGF-165,
 CC VEGF-189 AND VEGF-215).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC EMBL: M32977; G181971; -;
 DR EMBL: M27281; G340301; -;
 DR EMBL: M63978; G340215; JOINED.
 DR EMBL: M63971; G340215; JOINED.
 DR EMBL: M63972; G340215; JOINED.
 DR EMBL: M63973; G340215; JOINED.
 DR EMBL: M63974; G340215; JOINED.
 DR EMBL: M63975; G340215; JOINED.
 DR EMBL: M63976; G340215; JOINED.
 DR EMBL: M63977; G340215; JOINED.
 DR EMBL: X62568; G37659; -;
 DR PIR: A34492; A34492;
 DR PIR: A40079; A40079;
 DR PIR: A40080; A40080;
 DR PIR: A40454; A40454;
 DR PIR: B40454; B40454;
 DR PIR: C40454; C40454;
 DR PIR: J01463; J01463.

DR PIR: J01464; J01464.
 DR PIR: S17348; S17348.
 DR PDB: 1VGH; 08-APR-98.
 DR PDB: 2VGH; 08-APR-98.
 DR PDB: 1VPE; 08-APR-98.
 DR PDB: 2VPE; PRELIMINARY.
 DR MIM: 192240; -;
 DR PROSITE; PS00249; PDGF; 1.
 KW MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; ALTERNATIVE SPLICING; SIGNAL;
 KW 3D-STRUCTURE.
 FT SIGNAL 1 26
 FT CHAIN 27 215
 FT DISULFID 52 94
 FT DISULFID 83 128
 FT DISULFID 87 130
 FT DISULFID 77 77
 FT DISULFID 86 86
 FT CARBOHYD 101 101
 FT VARSPLIC 141 141
 FT VARSPLIC 142 165
 FT VARSPLIC 142 209
 SQ SEQUENCE 215 AA; 25173 MW; 18547894 CRC32;
 K -> N (IN VEGF-121 AND VEGF-165).
 MISSING (IN VEGF-165).
 MISSING (IN VEGF-121).
 Query Match 3.2%; Score 7; DB 1; Length 215;
 Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 91 GLECYPT 97
 Qy 85 GLECYPT 91
 RESULT 12
 ID EFN4 MOUSE STANDARD; PRT; 224 AA.
 AC 008542;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE EPHRIN-A4 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 4)
 DE (LEPR-4).
 GN EFN4 OR EPL4 OR LEPR4 OR EPL4.
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUKARYOTA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97060319.
 RA FLENNIKEN A.M., GALE N.W., YANCOPOULOS G.D., WILKINSON D.G.;
 RL DEV. BIOL. 179:382-401(1996).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
 CC EMBL: U90663; G1906017; -;
 DR MIM: MGI:106643; EFN4.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW GLYCOPROTEIN; GPI-ANCHOR; SIGNAL.
 FT SIGNAL 1 ?
 FT CHAIN ? 224
 FT CARBOHYD 51 51
 FT CARBOHYD 116 116
 FT SITE 59 61
 SQ SEQUENCE 224 AA; 24698 MW; D6908052 CRC32;
 CELL ATTACHMENT SITE (POTENTIAL).
 Query Match 3.2%; Score 7; DB 1; Length 224;
 Best Local Similarity 100.0%; Pred. No. 3.30e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 13 RPPAPG 19
 Qy 9 RPPAPG 15
 RESULT 13

BEST AVAILABLE

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ID Y146_HAEMIN STANDARD: PRT: 329 AA.
AC P44542.
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN H10146 PRECURSOR.
GN H10146.
OS HAEMOPHILUS INFLUENZAE.
OC PROKARYOTA: GRACILICUTES: SCOTOBACTERIA: FACULTATIVELY ANAEROBIC RODS:
OC PASTEURILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20.
RX MEDLINE: 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KEILAAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOGAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDER D.M., BRANDON R.C.,
RA FINE L.D., FRITZMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.;
RL SCIENCE 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC PROTEIN FAMILY 7.
DR EMBL: U32700: G1573102.
DR TIGR: H10146: -.
KW HYPOTHETICAL PROTEIN; TRANSPORT; PERIPLASMIC; SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 329 HYPOTHETICAL PROTEIN H10146.
SQ SEQUENCE 329 AA; 36513 MM; 84D68B15 CRC32;

Query Match 3.2% Score 7; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.30e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 64 YPSSOLG 70
OY 105 YPSSOLG 111

RESULT 14
ID SOX3_HUMAN STANDARD: PRT: 443 AA.
AC P41225; P35714;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE TRANSCRIPTION FACTOR SOX-3.
GN SOX3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94154672.
RA STEVANOVIC M., LOVELL-BADGE R., COLLIGNON J., GOODEFELLOW P.N.,
RL HUM. MOL. GENET. 2:2013-2018(1993).
RN [2]
RP SEQUENCE OF 150-203 FROM N.A.
RX MEDLINE: 92310993.
RA DENNY P., SMITH S., BRAND N., DABHADE N., BARTON P., ASHWORTH A.,
RL NUCLEIC ACIDS RES. 20:2887-2887(1992).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: CONTAINS 1 HMGB BOX.
CC -1- CAUTION: WAS CALLED SOX-9 BY REF. 2.
DR EMBL: X71135; G530020;
DR EMBL: X65665; G938234;
DR PIR: S21483; S21483.
DR PIR: S22942; S22942.
DR MIM: J13430;
KW DNA-BINDING; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION.

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FT DOMAIN 129 133 POLY-GLY.
FT DNA_BIND 139 207 HMGB BOX.
FT DOMAIN 234 248 POLY-ALA.
FT DOMAIN 290 294 POLY-PRO.
FT DOMAIN 321 327 POLY-ALA.
FT DOMAIN 337 344 POLY-ALA.
FT DOMAIN 350 361 POLY-ALA.
FT CONFLICT 159 159 L -> Q (IN REF. 2).
FT CONFLICT 176 176 D -> E (IN REF. 2).
FT CONFLICT 202 202 E -> D (IN REF. 2).
SQ SEQUENCE 443 AA; 44684 MM; FB8F7135 CRC32;

Query Match 3.2% Score 7; DB 1; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.30e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 57 APGASP 63
OY 155 APGASP 161

RESULT 15
ID COA2_BPPE3 STANDARD: PRT: 483 AA.
AC P03624;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-MAR-1989 (REL. 10, LAST ANNOTATION UPDATE)
DE MINOR COAT PROTEIN (ORF 483).
OS BACTERIOPHAGE PF3.
OC VIRIDAE; SS-DNA NONENVELOPED VIRUSES; INOVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW-YORK, AND NIJMEGEN.
RX MEDLINE: 85293231.
RA LUTTEN R.G.M., PUTERMAN D.G., SCHOENMAKERS J.G.G., KONINGS R.N.H.,
RA DAY L.A.;
RL J. VIROL. 56:268-276(1985).
CC -1- THE STRAIN NIJMEGEN SEQUENCE IS SHOWN.
DR EMBL: M11912; G215374;
DR EMBL: M19377; G215383;
DR PIR: A04232; VCBP13.
KW COAT PROTEIN.
FT VARIANT 419 419 L -> F (IN STRAIN NEW-YORK).
SQ SEQUENCE 483 AA; 52197 MM; 52AD1784 CRC32;

Query Match 3.2% Score 7; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.30e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 177 PRSYPGW 183
OY 146 PRSYPGW 152

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Search completed: Mon Nov 30 13:09:47 1998
Job time : 22 secs.

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MIPSBLH protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Nov 26 00:08:55 1998 MIPSBLH time 11.77 seconds

Tabular output not generated.

Title: UN-09-033-662-2

Description: (1-221) from G609033662.pep

Perfect Score: 221

Sequence: 1 MRRKSGRPAAPGVPAQA.....COGRGLMPPNCRRLAR 221

Scoring table: TABLE uniprottable

Gap 60

Searched: 120441 seqs, 3653193 residues

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database: MIPSBLH

Statistics: Mean 3.336; Variance 0.440; scale 7.535

Score No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

No. Score Match Length DB ID Description Pred. No.

1 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

2 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

3 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

4 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

5 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

6 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

7 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

8 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

9 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

10 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

11 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

12 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

13 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

14 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

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MIPSBLH

(TM)

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MIPSBLH protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Nov 26 00:08:55 1998 MIPSBLH time 11.77 seconds

Tabular output not generated.

Title: UN-09-033-662-2

Description: (1-221) from G609033662.pep

Perfect Score: 221

Sequence: 1 MRRKSGRPAAPGVPAQA.....COGRGLMPPNCRRLAR 221

Scoring table: TABLE uniprottable

Gap 60

Searched: 120441 seqs, 3653193 residues

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database: MIPSBLH

Statistics: Mean 3.336; Variance 0.440; scale 7.535

Score No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

No. Score Match Length DB ID Description Pred. No.

1 39 17.6 188 2 JC4680 Vascular endothelial 5.63e-88

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135	6	2	7	457	2	578281	hypothetical protein	5.00e+01
136	6	2	7	464	2	578831	hypothetical protein	5.00e+01
137	6	2	7	467	2	156896	gene gfi-2 protein -	5.00e+01
138	6	2	7	468	5	1587	serine protease (EC	5.00e+01
139	6	2	7	468	5	1587	serine protease (EC	5.00e+01
140	6	2	7	468	5	1587A	serine protease (EC	5.00e+01
141	6	2	7	471	2	518446	variant surface glyco	5.00e+01
142	6	2	7	475	2	56795	hypothetical protein	5.00e+01
143	6	2	7	482	2	56795	hypothetical protein	5.00e+01
144	6	2	7	486	1	56811	serine protease (EC	5.00e+01
145	6	2	7	487	2	56811	serine protease (EC	5.00e+01
146	6	2	7	493	2	56811	finger protein (clone	5.00e+01
147	6	2	7	501	1	56811	56k abortive late pro	5.00e+01
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150	6	2	7	507	2	574641	hypothetical protein	5.00e+01
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153	6	2	7	519	2	57414	halotylin R4 (EC 3.4	5.00e+01
154	6	2	7	529	2	44714	phosphoprotein phosph	5.00e+01
155	6	2	7	520	1	517868	alt-specific DNA met	5.00e+01
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209	6	217	643	1	F04306	gas polyprotein subunit 1	5-00e+01
210	6	217	679	2	S21764	heat shock protein 92	5-00e+01
211	6	217	681	2	178558	hypothetical Brachyur	5-00e+01
213	6	217	692	2	S53592	protein - kinase	5-00e+01
214	6	217	709	2	C28821	MRP1 protein	5-00e+01
215	6	217	711	2	S43464	1-phosphatidylinositol	5-00e+01
216	6	217	740	2	B55136	ecdysteroid-induced p	5-00e+01
217	6	217	745	2	B55136	coat protein YNP1 - rat	5-00e+01
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219	6	217	755	2	B78725	1-phosphatidylinositol	5-00e+01
220	6	217	756	2	S23942	phospholipase C delta	5-00e+01
221	6	217	759	2	S23942	phospholipase C delta	5-00e+01
222	6	217	783	1	A38637	Ras interactor RIL1	5-00e+01
223	6	217	790	2	A39627	protein-tyrosine kinase	5-00e+01
224	6	217	802	2	S45592	phosphatidylcholine	5-00e+01
225	6	217	803	2	S45592	phosphatidylcholine	5-00e+01
226	6	217	826	2	A60385	monocytic phospholipase	5-00e+01
227	6	217	836	2	S25218	pepC protein - Escher	5-00e+01
228	6	217	845	2	G08853	HCRP1 protein - human	5-00e+01
229	6	217	851	2	S11504	Dynamin - internal for	5-00e+01
230	6	217	852	2	S11504	Dynamin - internal for	5-00e+01
231	6	217	864	2	A40671	dynamin - internal for	5-00e+01
232	6	217	931	2	A64903	106 kD protein kinase	5-00e+01
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234	6	217	1028	1	C00034	gene p19equa4 protein	5-00e+01
235	6	217	1089	2	S66149	neural cell adhesion	5-00e+01
236	6	217	1143	2	129856	protein carboxypeptidase	5-00e+01
237	6	217	1145	2	S27114	guanine nucleotide-re	5-00e+01
238	6	217	1150	2	S27114	guanine nucleotide-re	5-00e+01
239	6	217	1244	2	S29083	nucleotide exchange f	5-00e+01
240	6	217	1250	2	S28407	4-alpha-glucosyltrans	5-00e+01
241	6	217	1251	2	S28407	4-alpha-glucosyltrans	5-00e+01
242	6	217	1258	1	P08875	amylo-1,6-glucosylase	5-00e+01
243	6	217	1552	2	A40203	neelin - rat	5-00e+01
244	6	217	1555	2	S39758	neelin - rat	5-00e+01
245	6	217	1556	2	S39758	neelin - rat	5-00e+01
246	6	217	1805	2	A49126	probable integral mem	5-00e+01
247	6	217	1808	2	A37361	probable integral mem	5-00e+01
248	6	217	1998	2	A35016	sodium channel protein	5-00e+01
249	6	217	2118	2	S64306	notch 3 protein - mou	5-00e+01
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251	6	217	2652	1	V01892	RNA-directed DNA polymerase	5-00e+01
252	6	217	2783	1	A19146	alpha-fetoprotein enh	5-00e+01
253	6	217	2783	1	A19146	collagen alpha 1(VI)	5-00e+01
254	6	217	3190	1	C00034	collagen alpha 1(VI)	5-00e+01
255	6	217	3199	1	C00034	collagen alpha 1(VI)	5-00e+01
256	6	217	3199	1	C00034	collagen alpha 1(VI)	5-00e+01

[illegible]

308	2	104	158E	antiserin mutant Q1E	1.45e+03
309	2	106	G5574	probable flagellat b1	1.45e+03
310	2	108	1Y7M1	ig lambda chain Fab f	1.45e+03
311	2	109	1Y7M2	ig lambda chain Fab f	1.45e+03
312	2	110	1Y7M3	RNA-directed DNA poly	1.45e+03
313	2	111	1HRB1	RNA-directed DNA poly	1.45e+03
314	2	112	1HRB2	ig heavy chain V reg1	1.45e+03
315	2	113	1HRB3	ig heavy chain V reg1	1.45e+03
316	2	114	1HRB4	ig heavy chain V reg1	1.45e+03
317	2	115	1HRB5	ig heavy chain V reg1	1.45e+03
318	2	116	1HRB6	ig heavy chain V reg1	1.45e+03
319	2	117	1HRB7	ig heavy chain V reg1	1.45e+03
320	2	118	1HRB8	ig heavy chain V reg1	1.45e+03
321	2	119	1HRB9	ig heavy chain V reg1	1.45e+03
322	2	120	1HRB10	ig heavy chain V reg1	1.45e+03
323	2	121	1HRB11	ig heavy chain V reg1	1.45e+03
324	2	122	1HRB12	ig heavy chain V reg1	1.45e+03
325	2	123	1HRB13	ig heavy chain V reg1	1.45e+03
326	2	124	1HRB14	ig heavy chain V reg1	1.45e+03
327	2	125	1HRB15	ig heavy chain V reg1	1.45e+03
328	2	126	1HRB16	ig heavy chain V reg1	1.45e+03
329	2	127	1HRB17	ig heavy chain V reg1	1.45e+03
330	2	128	1HRB18	ig heavy chain V reg1	1.45e+03
331	2	129	1HRB19	ig heavy chain V reg1	1.45e+03
332	2	130	1HRB20	ig heavy chain V reg1	1.45e+03
333	2	131	1HRB21	ig heavy chain V reg1	1.45e+03
334	2	132	1HRB22	ig heavy chain V reg1	1.45e+03
335	2	133	1HRB23	ig heavy chain V reg1	1.45e+03
336	2	134	1HRB24	ig heavy chain V reg1	1.45e+03
337	2	135	1HRB25	ig heavy chain V reg1	1.45e+03
338	2	136	1HRB26	ig heavy chain V reg1	1.45e+03
339	2	137	1HRB27	ig heavy chain V reg1	1.45e+03
340	2	138	1HRB28	ig heavy chain V reg1	1.45e+03
341	2	139	1HRB29	ig heavy chain V reg1	1.45e+03
342	2	140	1HRB30	ig heavy chain V reg1	1.45e+03
343	2	141	1HRB31	ig heavy chain V reg1	1.45e+03
344	2	142	1HRB32	ig heavy chain V reg1	1.45e+03
345	2	143	1HRB33	ig heavy chain V reg1	1.45e+03
346	2	144	1HRB34	ig heavy chain V reg1	1.45e+03
347	2	145	1HRB35	ig heavy chain V reg1	1.45e+03
348	2	146	1HRB36	ig heavy chain V reg1	1.45e+03
349	2	147	1HRB37	ig heavy chain V reg1	1.45e+03
350	2	148	1HRB38	ig heavy chain V reg1	1.45e+03
351	2	149	1HRB39	ig heavy chain V reg1	1.45e+03
352	2	150	1HRB40	ig heavy chain V reg1	1.45e+03
353	2	151	1HRB41	ig heavy chain V reg1	1.45e+03
354	2	152	1HRB42	ig heavy chain V reg1	1.45e+03
355	2	153	1HRB43	ig heavy chain V reg1	1.45e+03
356	2	154	1HRB44	ig heavy chain V reg1	1.45e+03
357	2	155	1HRB45	ig heavy chain V reg1	1.45e+03
358	2	156	1HRB46	ig heavy chain V reg1	1.45e+03
359	2	157	1HRB47	ig heavy chain V reg1	1.45e+03
360	2	158	1HRB48	ig heavy chain V reg1	1.45e+03
361	2	159	1HRB49	ig heavy chain V reg1	1.45e+03
362	2	160	1HRB50	ig heavy chain V reg1	1.45e+03
363	2	161	1HRB51	ig heavy chain V reg1	1.45e+03
364	2	162	1HRB52	ig heavy chain V reg1	1.45e+03
365	2	163	1HRB53	ig heavy chain V reg1	1.45e+03
366	2	164	1HRB54	ig heavy chain V reg1	1.45e+03
367	2	165	1HRB55	ig heavy chain V reg1	1.45e+03
368	2	166	1HRB56	ig heavy chain V reg1	1.45e+03
369	2	167	1HRB57	ig heavy chain V reg1	1.45e+03
370	2	168	1HRB58	ig heavy chain V reg1	1.45e+03
371	2	169	1HRB59	ig heavy chain V reg1	1.45e+03
372	2	170	1HRB60	ig heavy chain V reg1	1.45e+03
373	2				

359	5	2,3	150	5	1LNC	nucleoside diphosphat	1.45e+03
360	5	2,3	150	5	1LNC	nucleoside diphosphat	1.45e+03
361	2,3	150	5	1LWA	nucleoside diphosphat	1.45e+03	
362	2,3	150	5	1LWA	nucleoside diphosphat	1.45e+03	
363	2,3	150	5	1LWA	nucleoside diphosphat	1.45e+03	
364	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
365	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
366	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
367	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
368	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
369	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
370	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
371	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
372	2,3	150	5	1NDP	nucleoside diphosphat	1.45e+03	
373	2,3	152	5	1HBS	serine carboxypeptida	1.45e+03	
374	2,3	152	5	1HBS	serine type carboxype	1.45e+03	
375	2,3	152	5	1HBS	serine type carboxype	1.45e+03	
376	2,3	152	5	1HBS	serine type carboxype	1.45e+03	
377	2,3	153	5	1WIB	serine carboxypeptida	1.45e+03	
378	2,3	153	5	1WIB	nucleoside-diphosphat	1.45e+03	
379	2,3	153	5	661238	hypothetical protein	1.45e+03	
380	2,3	153	5	661238	hypothetical protein	1.45e+03	
381	2,3	156	5	1C23	cyclo periplasmic frag	1.45e+03	
382	2,3	159	5	1CIV	cyclo periplasmic frag	1.45e+03	
383	2,3	160	2	836369	serine type carboxype	1.45e+03	
384	2,3	160	2	1WIB	serine type carboxype	1.45e+03	
385	2,3	162	5	1HOG	methane monooxygenase	1.45e+03	
386	2,3	162	5	1HOG	methane monooxygenase	1.45e+03	
387	2,3	162	5	1MYG	methane monooxygenase	1.45e+03	
388	2,3	165	5	155544	peptonease binding pro	1.45e+03	
389	2,3	167	5	837721	hypothetical protein	1.45e+03	
390	2,3	167	5	837721	hypothetical protein	1.45e+03	
391	2,3	172	5	1PNY	phycoerythrin chain a	1.45e+03	
392	2,3	172	5	845051	variant luciferase-bin	1.45e+03	
393	2,3	174	5	845051	variant luciferase-bin	1.45e+03	
394	2,3	174	5	833750	male enhanced antigen	1.45e+03	
395	2,3	174	2	863234	isolectin 1,4,5-tripph	1.45e+03	
396	2,3	175	2	810333	hypothetical protein	1.45e+03	
397	2,3	178	5	845052	nucleotide gene compl	1.45e+03	
398	2,3	180	2	845052	nucleotide gene compl	1.45e+03	
399	2,3	180	2	845052	NAD dehydrogenase (u	1.45e+03	
400	2,3	184	2	864030	hypothetical protein	1.45e+03	
401	2,3	184	2	873197	ribosomal protein L22	1.45e+03	
402	2,3	186	5	8DRP	hypothetical protein	1.45e+03	
403	2,3	186	5	1ND7	dihydrofolate reducta	1.45e+03	
404	2,3	186	5	1ND6	dihydrofolate reducta	1.45e+03	
405	2,3	186	5	1ND6	dihydrofolate reducta	1.45e+03	
406	2,3	186	5	1ND3	dihydrofolate reducta	1.45e+03	
407	2,3	186	5	1ND5	dihydrofolate reducta	1.45e+03	
408	2,3	186	5	1ND5	dihydrofolate reducta	1.45e+03	
409	2,3	186	5	1ND2	dihydrofolate reducta	1.45e+03	

410	5	2.3	186	1	IMD1	dihydroxyacetate reductase	1.4e-003
411	5	2.3	187	5	IAO26	hla-drl class ii hist	1.4e-003
412	5	2.3	188	1	IAO27	hla-drl class ii hist	1.4e-003
413	5	2.3	189	1	IAO28	hla-drl class ii hist	1.4e-003
414	5	2.3	188	5	IAO29	hla-drl class ii hist	1.4e-003
415	2.3	188	5	1DHE	HMC class ix histocom	1.4e-003	
416	2.3	188	5	1DHE	HMC class ix histocom	1.4e-003	
417	2.3	190	5	56B230	antihistaminic peptide	1.4e-003	
418	2.3	190	5	56B230	antihistaminic peptide	1.4e-003	
419	2.3	192	5	1A58P	hla class ii histocom	1.4e-003	
420	2.3	193	5	6J3356	class ii histocompeti	1.4e-003	
421	2.3	193	5	6J3356	hypothetical protein	1.4e-003	
422	2.3	197	5	621010	pyridoxal synthase	1.4e-003	
423	2.3	197	5	621010	pyridoxal synthase	1.4e-003	
424	2.3	200	5	2PDC	proteolactonase 3.4-d	1.4e-003	
425	2.3	200	5	2PDC	proteolactonase 3.4-d	1.4e-003	
426	2.3	200	5	2PDC	proteolactonase 3.4-d	1.4e-003	
427	2.3	200	5	2PDC	proteolactonase 3.4-d	1.4e-003	
428	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
429	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
430	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
431	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
432	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
433	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
434	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
435	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
436	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
437	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
438	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
439	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
440	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
441	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
442	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
443	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
444	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
445	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
446	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
447	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
448	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
449	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
450	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
451	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
452	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
453	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
454	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
455	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
456	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
457	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
458	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
459	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	
460	2.3	200	5	3P6P	proteolactonase 3.4-d	1.4e-003	

461	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
462	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
463	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
464	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
465	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
466	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
467	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
468	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
469	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
470	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
471	5	2	3	200	2,032326	class II histocompat	1,45e+00
472	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
473	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
474	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
475	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
476	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
477	5	2	3	200	3P3C	protoproteaschute 3,4-4	1,45e+00
478	5	2	3	201	3P3C	protoproteaschute 3,4-4	1,45e+00
479	5	2	3	203	2,18368	caudal-type homeotic	1,45e+00
480	5	2	3	203	2,18368	caudal-type homeotic	1,45e+00
481	5	2	3	203	2,18368	caudal-type homeotic	1,45e+00
482	5	2	3	203	2,18368	caudal-type homeotic	1,45e+00
483	5	2	3	203	2,18368	caudal-type homeotic	1,45e+00
484	5	2	3	208	2,89366	conserved hypothetical	1,45e+00
485	5	2	3	210	5,176	immunoglobulin proteo	1,45e+00
486	5	2	3	210	5,176	immunoglobulin proteo	1,45e+00
487	5	2	3	210	5,176	immunoglobulin proteo	1,45e+00
488	5	2	3	210	5,176	immunoglobulin proteo	1,45e+00
489	5	2	3	210	5,176	immunoglobulin proteo	1,45e+00
490	5	2	3	211	1,11N	immunoglobulin proteo	1,45e+00
491	5	2	3	211	1,11N	immunoglobulin proteo	1,45e+00
492	5	2	3	211	1,11N	immunoglobulin proteo	1,45e+00
493	5	2	3	211	1,11N	immunoglobulin proteo	1,45e+00
494	5	2	3	212	1,11N	immunoglobulin proteo	1,45e+00
495	5	2	3	212	1,11N	immunoglobulin proteo	1,45e+00
496	5	2	3	212	1,11N	immunoglobulin proteo	1,45e+00
497	5	2	3	212	1,11N	immunoglobulin proteo	1,45e+00
498	5	2	3	212	1,11N	immunoglobulin proteo	1,45e+00
499	5	2	3	212	1,11N	immunoglobulin proteo	1,45e+00
500	5	2	3	212	1,11N	immunoglobulin proteo	1,45e+00
501	5	2	3	213	1,11N	immunoglobulin proteo	1,45e+00
502	5	2	3	213	1,11N	immunoglobulin proteo	1,45e+00
503	5	2	3	213	1,11N	immunoglobulin proteo	1,45e+00
504	5	2	3	213	1,11N	immunoglobulin proteo	1,45e+00
505	5	2	3	214	1,11N	immunoglobulin proteo	1,45e+00
506	5	2	3	214	1,11N	immunoglobulin proteo	1,45e+00
507	5	2	3	214	1,11N	immunoglobulin proteo	1,45e+00
508	5	2	3	215	1,11N	immunoglobulin proteo	1,45e+00
509	5	2	3	215	1,11N	immunoglobulin proteo	1,45e+00
510	5	2	3	215	1,11N	immunoglobulin proteo	1,45e+00
511	5	2	3	215	1,11N	immunoglobulin proteo	1,45e+00

512	512	2.3	216	1.8C3	hiv-1 reverse transcr	1.45e+00
511	511	2.3	217	5.8B/FH	PdV fragment of uninf	1.45e+00
510	510	2.3	218	9.4J136	ser protein - chicken	1.45e+00
509	509	2.3	219	1.8C3	15 gamma-1 chain V re	1.45e+00
508	508	2.3	220	1.8C3	15 gamma-1 chain V re	1.45e+00
507	507	2.3	221	1.8C3	Immunodeficiency vira	1.45e+00
506	506	2.3	222	1.8C3	2b5 fab variable reg	1.45e+00
505	505	2.3	223	1.8C3	2b5 fab variable reg	1.45e+00
504	504	2.3	224	1.8C3	2b5 fab variable reg	1.45e+00
503	503	2.3	225	1.8C3	2b5 fab variable reg	1.45e+00
502	502	2.3	226	1.8C3	2b5 fab variable reg	1.45e+00
501	501	2.3	227	1.8C3	2b5 fab variable reg	1.45e+00
500	500	2.3	228	1.8C3	2b5 fab variable reg	1.45e+00
499	499	2.3	229	1.8C3	2b5 fab variable reg	1.45e+00
498	498	2.3	230	1.8C3	2b5 fab variable reg	1.45e+00
497	497	2.3	231	1.8C3	2b5 fab variable reg	1.45e+00
496	496	2.3	232	1.8C3	2b5 fab variable reg	1.45e+00
495	495	2.3	233	1.8C3	2b5 fab variable reg	1.45e+00
494	494	2.3	234	1.8C3	2b5 fab variable reg	1.45e+00
493	493	2.3	235	1.8C3	2b5 fab variable reg	1.45e+00
492	492	2.3	236	1.8C3	2b5 fab variable reg	1.45e+00
491	491	2.3	237	1.8C3	2b5 fab variable reg	1.45e+00
490	490	2.3	238	1.8C3	2b5 fab variable reg	1.45e+00
489	489	2.3	239	1.8C3	2b5 fab variable reg	1.45e+00
488	488	2.3	240	1.8C3	2b5 fab variable reg	1.45e+00
487	487	2.3	241	1.8C3	2b5 fab variable reg	1.45e+00
486	486	2.3	242	1.8C3	2b5 fab variable reg	1.45e+00
485	485	2.3	243	1.8C3	2b5 fab variable reg	1.45e+00
484	484	2.3	244	1.8C3	2b5 fab variable reg	1.45e+00
483	483	2.3	245	1.8C3	2b5 fab variable reg	1.45e+00
482	482	2.3	246	1.8C3	2b5 fab variable reg	1.45e+00
481	481	2.3	247	2.822800	terminase gpM - phase	1.45e+00
480	480	2.3	248	4.831320	natural killer cell p	1.45e+00

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869	5	2,3	668	2	QJ1447	dark-type molecular c	1.45e+03	920	2,3	921	2	G02326	transcription factor	1.45e+03
870	2,3	670	2	QJ1447	NADH dehydrogenase (u	1.45e+03	921	2,3	922	2	S15304	peractin - Bordetella	1.45e+03	
871	2,3	670	2	QJ1447	NADH dehydrogenase (u	1.45e+03	922	2,3	923	2	S15380	progesterone receptor	1.45e+03	
872	2,3	671	2	QJ1447	transcription factor	1.45e+03	923	2,3	924	2	S15380	progesterone receptor	1.45e+03	
873	2,3	671	2	QJ1447	transcription factor	1.45e+03	924	2,3	925	2	S62929	male-specific lethal	1.45e+03	
874	2,3	674	2	852340	DNA ligase (Ado-) (EC	1.45e+03	925	2,3	926	2	S23408	prematurely terminate	1.45e+03	
875	2,3	677	2	8523296	collagen alpha 2(I)1	1.45e+03	926	2,3	980	2	854486	regulatory protein -	1.45e+03	
876	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	927	2,3	982	2	S23024	6-phosphogluconate	1.45e+03	
877	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	928	2,3	983	2	S23024	6-phosphogluconate	1.45e+03	
878	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	929	2,3	994	2	854486	leucine-tRNA ligase	1.45e+03	
879	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	930	2,3	1017	2	S13465	H1A protein - human	1.45e+03	
880	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	931	2,3	1018	2	S13465	H1A protein - human	1.45e+03	
881	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	932	2,3	1019	2	S13465	H1A protein - human	1.45e+03	
882	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	933	2,3	1024	2	S18351	entolipinase (EC 3	1.45e+03	
883	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	934	2,3	1024	2	S18351	entolipinase (EC 3	1.45e+03	
884	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	935	2,3	1024	2	S18351	entolipinase (EC 3	1.45e+03	
885	2,3	678	5	17KRA	transketolase (EC 2.2	1.45e+03	936	2,3	1024	2	S18351	entolipinase (EC 3	1.45e+03	
886	2,3	682	2	851349	probable vitron protei	1.45e+03	937	2,3	1041	2	A52684	15X outer membrane p	1.45e+03	
887	2,3	682	2	851349	probable vitron protei	1.45e+03	938	2,3	1056	1	DNA551	DNA-directed DNA poly	1.45e+03	
888	2,3	682	2	851349	probable vitron protei	1.45e+03	939	2,3	1056	1	DNA551	DNA-directed DNA poly	1.45e+03	
889	2,3	685	2	11552	dRNA-binding protein	1.45e+03	940	2,3	1061	2	DNA12	DNA-directed DNA poly	1.45e+03	
890	2,3	689	2	A16573	long-chain fatty-acid	1.45e+03	941	2,3	1062	2	A46869	mitotic protein klp1	1.45e+03	
891	2,3	689	2	A16573	long-chain fatty-acid	1.45e+03	942	2,3	1066	2	A46869	mitotic protein klp1	1.45e+03	
892	2,3	700	2	A12392	protein kinase C (EC	1.45e+03	943	2,3	1072	2	A37327	microtubule-associate	1.45e+03	
893	2,3	701	2	D48613	gag polyprotein - Mye	1.45e+03	944	2,3	1075	2	A57317	transcription factor	1.45e+03	
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895	2,3	704	2	A43599	transcriptional initiat	1.45e+03	946	2,3	1093	2	A12356	transcription factor	1.45e+03	
896	2,3	704	2	A43599	transcriptional initiat	1.45e+03	947	2,3	1093	2	A12356	transcription factor	1.45e+03	
897	2,3	718	2	873088	glycogen octon prote	1.45e+03	948	2,3	1099	2	A56455	tumor suppressor prot	1.45e+03	
898	2,3	718	2	873088	glycogen octon prote	1.45e+03	949	2,3	1099	2	A56455	tumor suppressor prot	1.45e+03	
899	2,3	723	2	873088	glycogen octon prote	1.45e+03	950	2,3	1117	2	863199	probable membrane pro	1.45e+03	
900	2,3	723	2	873088	glycogen octon prote	1.45e+03	951	2,3	1120	2	863199	probable membrane pro	1.45e+03	
901	2,3	723	2	873088	glycogen octon prote	1.45e+03	952	2,3	1120	2	863199	probable membrane pro	1.45e+03	
902	2,3	723	2	873088	glycogen octon prote	1.45e+03	953	2,3	1120	2	863199	probable membrane pro	1.45e+03	
903	2,3	723	2	873088	glycogen octon prote	1.45e+03	954	2,3	1120	2	863199	probable membrane pro	1.45e+03	
904	2,3	723	2	873088	glycogen octon prote	1.45e+03	955	2,3	1120	2	863199	probable membrane pro	1.45e+03	
905	2,3	723	2	873088	glycogen octon prote	1.45e+03	956	2,3	1120	2	863199	probable membrane pro	1.45e+03	
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907	2,3	723	2	873088	glycogen octon prote	1.45e+03	958	2,3	1120	2	863199	probable membrane pro	1.45e+03	
908	2,3	723	2	873088	glycogen octon prote	1.45e+03	959	2,3	1120	2	863199	probable membrane pro	1.45e+03	
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911	2,3	723	2	873088	glycogen octon prote	1.45e+03	962	2,3	1120	2	863199	probable membrane pro	1.45e+03	
912	2,3	723	2	873088	glycogen octon prote	1.45e+03	963	2,3	1120	2	863199	probable membrane pro	1.45e+03	
913	2,3	723	2	873088	glycogen octon prote	1.45e+03	964	2,3	1120	2	863199	probable membrane pro	1.45e+03	
914	2,3	723	2	873088	glycogen octon prote	1.45e+03	965	2,3	1120	2	863199	probable membrane pro	1.45e+03	
915	2,3	723	2	873088	glycogen octon prote	1.45e+03	966	2,3	1120	2	863199	probable membrane pro	1.45e+03	
916	2,3	723	2	873088	glycogen octon prote	1.45e+03	967	2,3	1120	2	863199	probable membrane pro	1.45e+03	
917	2,3	723	2	873088	glycogen octon prote	1.45e+03	968	2,3	1120	2	863199	probable membrane pro	1.45e+03	
918	2,3	723	2	873088	glycogen octon prote	1.45e+03	969	2,3	1120	2	863199	probable membrane pro	1.45e+03	
919	2,3	723	2	873088	glycogen octon prote	1.45e+03	970	2,3	1120	2	863199	probable membrane pro	1.45e+03	

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RESULT 6
ENTRY 557956
TITLE ovine vascular endothelial growth factor - sheep
ORGANISM Ovis montanus
DATE 13-Jan-1996
ACCESSIONS 557956
REFERENCES 557956
AUTHORS D. A. Del Y. L. J. Jones, S. C. Moor, R. M.
SUBMISSION 557956
REVISION 557956
*molecule-type mRNA
*accession 557956
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DB 137 CERNPK 137
CY 131 CERNPK 137

RESULT 7
ENTRY 837806
TITLE nitric oxide hydratase (EC 4.2.1.84) alpha chain - Brevibacterium
ORGANISM Brevibacterium sp.
DATE 14-Jun-1997
ACCESSIONS 837806
REFERENCES 837806
AUTHORS Mayeux, J. P.; Cerbasi, E.; Soubrier, F.; Faucher, D.;
*journal J. Biol. Chem. (1997) 272:6764-6773
*title Purification, cloning, and primary structure of an
*abstract R133: structural evidence for genetic coupling with nitric
*accession NM0029107222
*checksum 837806
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DB 137 CERNPK 137
CY 131 CERNPK 137

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Query Match 3.24: Score 7; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 9.45e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 14 PLOAFVS 20
CY 17 PLOAFVS 23

RESULT 8
ENTRY 840080
TITLE vascular endothelial growth factor precursor (version 2) -
ORGANISM Bos taurus
DATE 30-Jun-1997
ACCESSIONS 840080
REFERENCES 840080
AUTHORS Perreux, N.; Carhane, G.; Kung, W. J.; Goeddel, D. V.;
*journal Science (1997) 276:1306-1309
*title Vascular endothelial growth factor is a secreted angiogenic
*accession U00080
*molecule-type mRNA
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*length 1190
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*checksum 840080
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DB 137 CERNPK 137
CY 131 CERNPK 137

RESULT 11
ENTRY 844881
TITLE vascular endothelial growth factor-1 precursor - mouse
ORGANISM Mus musculus
DATE 10-Sep-1997
ACCESSIONS 844881
REFERENCES 844881
AUTHORS Brister, G. J.; Altschul, G. J.; Sanger, S. J.; Rhee, W.;
*journal Proc. Natl. Acad. Sci. U.S.A. (1997) 94:1515-1519
*title Expression of vascular endothelial growth factor during
*abstract embryonic angiogenesis and endothelial cell
*accession U00080
*molecule-type mRNA
*accession 844881
*length 1190
*molecular-weight 13006
*checksum 844881
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Best Local Similarity 100.0%; Pred. No. 9.45e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 137 CERNPK 137
CY 131 CERNPK 137

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PLANTINE
ENTRY 371390
TITLE domain signal sequence aspartate predicted label 5100
ORGANISM Arabidopsis thaliana
DATE 13-Jan-1996
ACCESSIONS 371390
REFERENCES 371390
AUTHORS
*journal J. Biol. Chem. (1996) 271:10764-10773
*title Purification, cloning, and primary structure of an
*abstract R133: structural evidence for genetic coupling with nitric
*accession NM0029107222
*checksum 371390
*molecule-type DNA
*accession 371390
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Best Local Similarity 100.0%; Pred. No. 9.45e-01;
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DB 137 CERNPK 137
CY 131 CERNPK 137

RESULT 9
ENTRY 552110
TITLE ovine vascular endothelial growth factor - pig
ORGANISM Ovis montanus
DATE 14-Jul-1995
ACCESSIONS 552110
REFERENCES 552110
AUTHORS Sharma, H. S.; Tang, Z. H.; Cho, B. C. G.; Verduyn, P. D.;
*journal Biochem. Biophys. Acta (1995) 1260:233-238
*title Nucleotide sequence and expression of the porcine vascular
*abstract endothelial growth factor.
*accession 552110
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*checksum 1576
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CY 85 CERNPK 91

RESULT 10
ENTRY A13987
TITLE plasma-derived vascular endothelial cell growth factor - rat
ORGANISM Rattus norvegicus
DATE 16-Nov-1990
ACCESSIONS A13987

REFERENCE A13987
AUTHORS Comp, G. J.; Bayne, M. L.; Sodeman, D. D.; Kwoh, P. W.; Sullivan,
K. A.; Pallas, T. M.; Hope, D. A.; Thomas, R. A.;
*journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7628-7632
*title Amino acid and cDNA sequence of a vascular endothelial cell
*abstract growth factor that is homologous to platelet-derived growth
*accession A13987
*accession A13987
*length 190
*molecular-weight 2336
*checksum 1947
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DB 137 CERNPK 137
CY 131 CERNPK 137

RESULT 11
ENTRY 844881
TITLE vascular endothelial growth factor-1 precursor - mouse
ORGANISM Mus musculus
DATE 10-Sep-1997
ACCESSIONS 844881
REFERENCES 844881
AUTHORS Brister, G. J.; Altschul, G. J.; Sanger, S. J.; Rhee, W.;
*journal Proc. Natl. Acad. Sci. U.S.A. (1997) 94:1515-1519
*title Expression of vascular endothelial growth factor during
*abstract embryonic angiogenesis and endothelial cell
*accession U00080
*molecule-type mRNA
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*length 1190
*molecular-weight 13006
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Query Match 3.24: Score 7; DB 2; Length 1190;
Best Local Similarity 100.0%; Pred. No. 9.45e-01;
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DB 137 CERNPK 137
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#note NCBI:110665; derived from NCBI database (NCBI:110665,
NDB:P110675)
REFERENCE
  authors Rosenblatt, R.A.; Megyesi, T.F.; Henzel, W.J.; Ferrara, N.;
  Ascioglu, A.
  journal Growth Factors (1990) 4:51-59
  title Conditioned medium from mouse fatcrom 180 cells contains
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  accession J01000
  molecular_type Protein
  keywords #protein, #signal, #os
  alternative_splittings angiogenesis; dimer; disulfide bond;
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CY 121 GENEEXP 127

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  ORGANISM Hordeum vulgare L. [Eukaryota]
  DATE 03-Jun-1993 sequence_version 30-Sep-1993 seq_change
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  ACCESSION R145512
  REFERENCE R145512
  journal Cattellvelli, L.; Barreis, D.
  title Plant Physiol. (1990) 93:1504-1510
  title Molecular cloning and characterization of cold-regulated
    protein in barley.
  accession R145512
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  #molecule_type mRNA
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[illegible]

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ORGANISM Rhodococcus erythropolis
DATE     14-Jul-1994
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        10-Sep-1997
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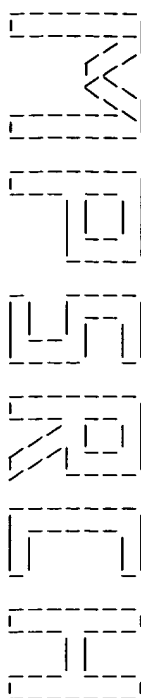
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PATRONS carbon-oxygen lyase; hydro-lyase
SUMMARY
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length 207 molecular-weight 22996 ecnumber 3749
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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Cv 17 PROPAIR 23
RESULTS
RESULT 15
TITLE Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation
CONTAINS
DATE
ORIGIN DRAKE
REFERENCE A44681: C64681; A60932; S53136
ACCESSIONS A44681
JOURNAL Bracton, G.; Albright, U.; Steyer, S.; Rissau, W.
Title Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation
cross-reference NCBI:5724850
Accession A44681
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#molecule_type RNA
#residues 209-314 #label BR2
#comment Sequence extracted from NCBI backbone (NCBI:107624, NCBI:107625)
REFERENCE A60931
AUTHORS Fahlstedt, P.C.; Palm, I.C.E.; Olander, J.V.; Connolly,

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Journal J. Exp. Med. (1990) 172:1535-1545
Title Vascular permeability factor: a tumor-derived polypeptide
that induces endothelial cell and monocyte procoagulant
activity, and promotes monocyte migration.
Accession A60937
Molecule-type protein
Residues 37-33 *label C1A
REFERENCE
55116
Accession J. Exp. Med. (1990) 172:1535-1545
Journal Biochim. Biophys. Acta (1994) 1224:165-170
Title Enhanced expression of multiple forms of VEGF is associated
with spontaneous immortalization of murine fibroblasts.
Accession 55116
Molecule-type protein
Residues 37-46 *label SUG
COMMENT Homologs could be demonstrated for recombinant VEGF-2 but not
VEGF-1
KEYWORDS VEGF-1 alternative splicing; angiogenesis; disulfide bond;
glycoprotein; homodimer; mitogen
FEATURE
1-26 domain signal sequence status predicted label SIG
17-214 domain signal sequence status predicted label SIG
SIGNAL
length 214 molecular-weight 25283 checksum 2404
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Matches 71 Similarity 100.0% Seq ID 100.0%
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QY 121 CCEPRK 127
Search completed: Thu Nov 26 00:10:58 1998
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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Nov 30 13:08:17 1998; MasPar time 7.61 Seconds
Tabular output not generated. 469,670 Million cell updates/sec

Title: >US-09-033-662-2
Description: (1-221) from US09033662.pep
Perfect Score: 221
Sequence: 1 MRCRISGRPPAPGPVPAQA.....COGRGLELNPDCRCKRLRR 221

Scoring table:
Gap 60
TABLE uninterpretable

Searched: 131922 seqs, 16180660 residues
Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 2.708; Variance 0.678; scale 3.995

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result *Beny*
No. Score Match length DB ID Description Pred. No.

No.	Score	Match length	DB	ID	Description	Pred. No.
1	221	100	0	221 23	W07611 Human vascular endoth	0.09e+00
2	149	67	4	207 21	W04831 Vascular endothelial	3.09e-233
3	149	67	4	207 19	W00725 Vascular endothelial	3.09e-233
4	120	54	3	143 19	W00727 Vascular endothelial	7.62e-184
5	119	53	8	188 19	W00726 Vascular endothelial	3.81e-182
6	119	53	8	188 21	W04829 Fibrosarcoma vascular	3.81e-182
7	83	37	6	101 19	W00728 Vascular endothelial	3.21e-121
8	39	17	6	102 21	W04824 Vascular endothelial	4.35e-48
9	39	17	6	133 21	W04828 Vascular endothelial	4.35e-48
10	39	17	6	188 21	W04826 Heart vascular endoth	4.35e-48
11	39	17	6	188 19	W00864 Murine VRF167.	4.35e-48
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14	35	15	8	195 21	W04827 Heart vascular endoth	1.32e-41
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16	17	7	7	55 21	W04825 Vascular endothelial	2.02e-13
17	8	3	6	13 21	W04823 Consensus sequence fo	6.17e-01
18	7	3	2	12 23	W23803 VEGF/VpF antigen sequ	9.57e+00

19	7	3	2	65 18	R94035 VEGF exon III.	9.57e+00
20	7	3	2	120 7	R38916 Bovine VEGF-120.	9.57e+00
21	7	3	2	121 27	W40597 VEGF/VPEF121.	9.57e+00
22	7	3	2	121 20	W09091 Human VEGF/VPEF121 for	9.57e+00
23	7	3	2	121 17	R96043 Human vascular permea	9.57e+00
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52	7	3	2	190 2	R27352 Bovine vascular endoth	9.57e+00
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59	7	3	2	191 19	W00724 VEGF165 Cys+2.	9.57e+00
60	7	3	2	192 18	R94040 VEGF165 Cys+4.	9.57e+00
61	7	3	2	192 18	R94039 VEGF165 Cys+4.	9.57e+00
62	7	3	2	214 4	R22351 Alternative form of V	9.57e+00
63	7	3	2	215 16	R91077 Human vascular endoth	9.57e+00
64	7	3	2	215 18	R94003 Human vascular pemea	9.57e+00
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81	7	3	2	539 27	W38236 VEGF/CPG2 fusion prot	9.57e+00
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92 7 3.2 612 18 W00596 SAP(Gly4Ser)2VEGF165(9.57e+00
93 7 3.2 640 3 R15436 Alpha-1,6-glycan-6-91 9.57e+00
94 7 3.2 646 29 W55314 H. pylori ORF hpj138 9.57e+00
95 7 3.2 818 27 W5297 Human islet cell anti 9.57e+00
96 7 3.2 876 23 W18091 Type I diabetes-asso 9.57e+00
97 7 3.2 969 24 W25170 Human insulinoma-asso 9.57e+00
98 7 3.2 1012 27 W5296 Macaque islet cell an 9.57e+00
99 7 3.2 1015 27 W5345 Human protein tyrosin 9.57e+00
100 7 3.2 1015 23 W18092 Type I diabetes-asso 9.57e+00

ALIGNMENTS

RESULT 1
ID W07611 standard; Protein: 221 AA.
AC W07611:
DE 01-SEP-1997 (first entry)
KW Human vascular endothelial growth factor 3.
KW Human vascular endothelial growth factor; hVEGF3; angiogenesis;
KW tumour; inflammation; rheumatoid arthritis; diabetic retinopathy;
KW psoriasis; bone; periodontium; ligament; antagonist.
OS Homo sapiens.
FH key
FT region
FT 69..82 Location/Qualifiers
FT /label= "PDGF/VEGF family signature
FT /note= "conserved PXCXXXXXRGCCN motif"
PN W0639421-A1.
PN 12-DEC-1996.
PR 06-JUN-1995; U07283.
PR 06-JUN-1995; W0-U07283.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Olsen H, Rosen CA, Hu JS;
PI WPI: 97-043056/04.
DR N-PSDB: T44071.
PT DNA encoding human vascular endothelial growth factor 3 - useful to
PT develop prods. for, e.g. stimulating angiogenesis or treating
PT tumours, inflammation or rheumatoid arthritis
PS Claim 11; Page 44; 56pp; English.
CC This sequence is that of human vascular endothelial growth factor 3
CC (VEGF3). The growth factor can be used to stimulate angiogenesis and
CC wound healing, and to promote vascular tissue repair. It can also be
CC used to induce the growth of damaged bone, periodontium or ligament
CC tissue. VEGF3 antagonists can be used to inhibit tumour growth, or to
CC treat diabetic retinopathy, inflammation, rheumatoid arthritis or
CC psoriasis. VEGF3 is structurally related to the PDGF/VEGF family
CC and it includes the conserved signature motif for the family (see
CC features table).
SQ Sequence 221 AA:

Query Match 100.0%; Score 221; DB 23; Length 221;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MRCRISGRPAPPGVPAQAPVSGPDAHQKRVSWIDYTRATCPRREVVLTVELM 60
QY 1 MRCRISGRPAPPGVPAQAPVSGPDAHQKRVSWIDYTRATCPRREVVLTVELM 60
Db 61 GTAKQLVPSCTVIVORCGGCCPDGELCVPTGQHOVMQILMIRYPSQLEMSLEHSQ 120
QY 61 GTAKQLVPSCTVIVORCGGCCPDGELCVPTGQHOVMQILMIRYPSQLEMSLEHSQ 120
Db 121 CECRPPKKSAAVPAKPAATPHRPPQPSVPGVWDSAPAPSPADITGSHSPRLPCPTQ 180
QY 121 CECRPPKKSAAVPAKPAATPHRPPQPSVPGVWDSAPAPSPADITGSHSPRLPCPTQ 180
Db 181 HHQCPDPRTCRCRCRRSRFLRCOGRIELNPDTCRCRKLRR 221
QY 181 HHQCPDPRTCRCRCRRSRFLRCOGRIELNPDTCRCRKLRR 221

RESULT 2
ID W04831 standard; Protein: 207 AA.
AC W04831:

DT 28-APR-1997 (first entry)
DE Vascular endothelial growth factor-B186.
KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
OS Homo sapiens.
FH key
FT region
FT 69..82 Location/Qualifiers
FT /label= "PDGF/VEGF family signature
FT /note= "conserved PXCXXXXXRGCCN motif"
PN W0639421-A1.
PN 12-DEC-1996.
PR 06-JUN-1995; U07283.
PR 06-JUN-1995; W0-U07283.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Olsen H, Rosen CA, Hu JS;
PI WPI: 97-043056/04.
DR N-PSDB: T44071.
PT DNA encoding human vascular endothelial growth factor 3 - useful to
PT develop prods. for, e.g. stimulating angiogenesis or treating
PT tumours, inflammation or rheumatoid arthritis
PS Claim 11; Page 44; 56pp; English.
CC This sequence is that of human vascular endothelial growth factor 3
CC (VEGF3). The growth factor can be used to stimulate angiogenesis and
CC wound healing, and to promote vascular tissue repair. It can also be
CC used to induce the growth of damaged bone, periodontium or ligament
CC tissue. VEGF3 antagonists can be used to inhibit tumour growth, or to
CC treat diabetic retinopathy, inflammation, rheumatoid arthritis or
CC psoriasis. VEGF3 is structurally related to the PDGF/VEGF family
CC and it includes the conserved signature motif for the family (see
CC features table).
SQ Sequence 221 AA:

Query Match 67.4%; Score 149; DB 21; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.09e-233;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 PAAQAPVSGDAPDAPGKRVSWIDYTRATCQPREVVPLTVELMGTVAQLVPSCTVQR 77
QY 17 PAAQAPVSGDAPDAPGKRVSWIDYTRATCQPREVVPLTVELMGTVAQLVPSCTVQR 76
Db 78 CGGCGPDDELCEVPTGQHOVMQILMIRYPSQLEMSLEHSQCCRCRKKDSAVKPR 136
QY 77 CGGCGPDDELCEVPTGQHOVMQILMIRYPSQLEMSLEHSQCCRCRKKDSAVKPR 136
Db 138 AATPHRPPQPSVPGVWDSAPAPSPADIT 165
QY 137 AATPHRPPQPSVPGVWDSAPAPSPADIT 165

RESULT 3
ID W00725 standard; Protein: 207 AA.
AC W00725:
DE 30-NOV-1996 (first entry)
KW Vascular endothelial growth factor-1 like protein SOM175.
KW Vascular endothelial growth factor; VEGF; VEGF165; SOM175; neuron;
KW astroglial proliferation.
OS Homo sapiens.
FH key
FT region
FT 69..82 Location/Qualifiers
FT /label= "sig_peptide

PN W09627007-A1.
 PD 06-SEP-1996.
 PR 22-FEB-1996: AU0094.
 PR 02-MAR-1995: AU-001457.
 PR 20-NOV-1995: AU-006647.
 PR 22-DEC-1995: AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
 PI Weber G;
 DR N-PSDB: T33610.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 survival
 PS Claim 11: Page 41; 113pp; English.
 CC Human vascular endothelial growth factor (VEGF)-like polypeptide
 CC (W00725) is capable of inducing the proliferation of vascular
 CC endothelial cells, of interacting with flt-1/Krl-1 receptors,
 CC and of inducing cell migration, cell survival and/or an increase
 CC in intracellular levels of alkaline phosphatase. It shows 33.3%
 CC identity with human VEGF (see also W00724). Splice variants
 CC (W00726-28) of SOM175 have also been identified. Recombinant SOM175
 CC can be produced in host cells transformed with vectors carrying
 CC SOM175 cDNA (see also T33610). It is useful for inducing astroglial
 CC proliferation and for promoting neural survival and/or proliferation.
 SQ Sequence 207 AA;
 Query Match 67.4%; Score 149; DB 19; Length 207;
 Best Local Similarity 100.0%; Pred. No. 3.09e-233;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 pagapvsgdapgqhrkxvswldytracqprevvplvtelngtvakqlvpscvtvqr 77
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 QY 17 PAQAPVSPDAPGHRKRVSWIDYTRATCPREVVPLVTELMGTAKQLVPCSVTVQR 76
 |||||||
 Db 78 cggccpddgilecvtgqhvrmqllmtrypsqdgemslehsqecrpkkkdsavkpr 137
 |||||||
 QY 77 CGGCCPDGLEGCVPTGQHVQMQLMIRYPSQJGEMSLHESQCECRPKKDSAVKPR 136
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 Db 138 aatphrprprrvsgwdsapgapspadit 166
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 QY 137 AATPHRRPQRSVPCWDSAPGAPSPADIT 165
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 RESULT 4
 ID W00727 standard; Protein: 143 AA.
 AC W00727:
 DT 30-NOV-1996 (first entry)
 DE Vascular endothelial growth factor-like protein SOM175-e6+e7.
 KW Vascular endothelial growth factor; VEGF; SOM175-e6+e7; neuron;
 KW astroglial proliferation.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..21
 FT /label= sig-peptide
 PN W09627007-A1.
 PD 06-SEP-1996.
 PR 22-FEB-1996: AU0094.
 PR 02-MAR-1995: AU-001457.
 PR 20-NOV-1995: AU-006647.
 PR 22-DEC-1995: AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
 PI Weber G;
 DR N-PSDB: T33612.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 survival
 PS Claim 13: Page 46; 113pp; English.
 CC Splice variants (W00726-28) of the human vascular endothelial growth
 CC factor-like polypeptide SOM175 (see also W00725) are products of
 CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
 CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at
 CC least 1 of the properties of SOM175 including the ability to induce
 CC proliferation of vascular endothelial cells, to interact with
 CC flt-1/Krl-1 receptors, and to induce cell migration, cell survival
 CC and/or an increase in intracellular levels of alkaline phosphatase.
 CC Recombinant SOM175 proteins can be used to induce astroglial
 CC proliferation and to promote neural survival and/or proliferation.
 SQ Sequence 188 AA;
 Query Match 53.8%; Score 119; DB 19; Length 188;
 Best Local Similarity 100.0%; Pred. No. 3.81e-182;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 pagapvsgdapgqhrkxvswldytracqprevvplvtelngtvakqlvpscvtvqr 77
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 QY 17 PAQAPVSPDAPGHRKRVSWIDYTRATCPREVVPLVTELMGTAKQLVPCSVTVQR 76
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 Db 78 cggccpddgilecvtgqhvrmqllmtrypsqdgemslehsqecrpkkkdsavkpr 136
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 QY 77 CGGCCPDGLEGCVPTGQHVQMQLMIRYPSQJGEMSLHESQCECRPKKDSAVKPR 135
 |||||||

CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at
 CC least 1 of the properties of SOM175 including the ability to induce
 CC proliferation of vascular endothelial cells, to interact with
 CC flt-1/Krl-1 receptors, and to induce cell migration, cell survival
 CC and/or an increase in intracellular levels of alkaline phosphatase.
 CC Recombinant SOM175 proteins can be used to induce astroglial
 CC proliferation and to promote neural survival and/or proliferation.
 SQ Sequence 143 AA;
 Query Match 54.3%; Score 120; DB 19; Length 143;
 Best Local Similarity 100.0%; Pred. No. 7.62e-184;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 17 PAQAPVSPDAPGHRKRVSWIDYTRATCPREVVPLVTELMGTAKQLVPCSVTVQR 76
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 Db 78 cggccpddgilecvtgqhvrmqllmtrypsqdgemslehsqecrpkkkdsavkpr 137
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 QY 77 CGGCCPDGLEGCVPTGQHVQMQLMIRYPSQJGEMSLHESQCECRPKKDSAVKPR 136
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 RESULT 5
 ID W00726 standard; Protein: 188 AA.
 AC W00726:
 DT 30-NOV-1996 (first entry)
 DE Vascular endothelial growth factor-like protein SOM175-e6.
 KW Vascular endothelial growth factor; VEGF; SOM175-e6; neuron;
 KW astroglial proliferation.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..21
 FT /label= sig-peptide
 PN W09627007-A1.
 PD 06-SEP-1996.
 PR 22-FEB-1996: AU0094.
 PR 02-MAR-1995: AU-001457.
 PR 20-NOV-1995: AU-006647.
 PR 22-DEC-1995: AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
 PI Weber G;
 DR N-PSDB: T33611.
 DR N-PSDB: T33611.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 survival
 PS Claim 12: Page 42-43; 113pp; English.
 CC Splice variants (W00726-28) of the human vascular endothelial growth
 CC factor-like polypeptide SOM175 (see also W00725) are products of
 CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
 CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at
 CC least 1 of the properties of SOM175 including the ability to induce
 CC proliferation of vascular endothelial cells, to interact with
 CC flt-1/Krl-1 receptors, and to induce cell migration, cell survival
 CC and/or an increase in intracellular levels of alkaline phosphatase.
 CC Recombinant SOM175 proteins can be used to induce astroglial
 CC proliferation and to promote neural survival and/or proliferation.
 SQ Sequence 188 AA;
 Query Match 53.8%; Score 119; DB 19; Length 188;
 Best Local Similarity 100.0%; Pred. No. 3.81e-182;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 18 pagapvsgdapgqhrkxvswldytracqprevvplvtelngtvakqlvpscvtvqr 77
 |||||||
 QY 17 PAQAPVSPDAPGHRKRVSWIDYTRATCPREVVPLVTELMGTAKQLVPCSVTVQR 76
 |||||||
 Db 78 cggccpddgilecvtgqhvrmqllmtrypsqdgemslehsqecrpkkkdsavkpr 136
 |||||||
 QY 77 CGGCCPDGLEGCVPTGQHVQMQLMIRYPSQJGEMSLHESQCECRPKKDSAVKPR 135
 |||||||

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RESULT 6
ID W04829 standard; Protein; 188 AA.
AC W04829;
DT 28-APR-1997 (first entry)
DE Fibrosarcoma vascular endothelial growth factor-B167.
KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW Vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
OS Homo sapiens.
PN W09627007-41.
PD 06-SEP-1996.
PF 01-MAR-1996; 002957.
PR 01-MAR-1995; US-397651.
PR 06-JUN-1995; US-469427.
PR 06-DEC-1995; US-569063.
PA (LUDM-) LUDMIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
PI WPI: 96-412582/41.
DR N-PSDB: T37913.
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
PS Claim 18; Page 59; 107pp; English.
CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which it
CC is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting endothelial
CC cell growth during normal embryonic development, wound healing, and
CC tissue regeneration/reorganisation. The VEGF proteins of the invention
CC share the angiogenic and other properties of VEGF, but are distributed
CC and expressed in tissues differently to VEGF. The proteins can therefore
CC be used to accelerate angiogenesis in wound healing. Antibodies against
CC the proteins can be used for inhibiting angiogenesis. The antibodies can
CC also be used diagnostically to quantitatively detect VEGF-B. Primers
CC complementary to the coding sequences for the proteins of the invention
CC can also be used to detect VEGF-B coding sequences. Quantification of
CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
CC metastatic risk. VEGF-B expression in a cell can be retarded using
CC antisense sequences direct against the VEGF coding sequences, this is
CC especially useful in retarding VEGF expression in tumour cells.
SQ Sequence 188 AA;

Query Match 53.8%; Score 119; DB 21; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.81e-182;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 18 pagavsqdapgqhrkvsvdytracqprevvplvtelmgvtakqlpvcstvtgr 77
AC W04824;
DT 17 PAQAVSQPDAGHQRKRVSWIDVTRATCPREVVPVLTVELMGVAKOLVPSCTVOR 76
OY
DB 78 cggccpddgdlccvptgqhvrmqimlirpssqigemsleehsqcecrpkkkdsavxdp 136
OY 77 CGGCCPDGDLCCVPTGQHVQVRMQLMIRPSSQLGEMSLHSHSCCECRPKKDSAVKPD 135

RESULT 7
ID W00728 standard; Protein; 101 AA.
AC W00728;
DT 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175-e4.
KW Vascular endothelial growth factor; VEGF; SOM175-e4; neuron;
KW Astroglial proliferation.
OS Homo sapiens.
PN Key location/Qualifiers
FT Key 1.21
FT peptide /label= Sig_peptide
PN W09627007-41.

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PD 06-SEP-1996.
PF 22-FEB-1996; AU0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
PI WPI: 96-412774/41.
DR N-PSDB: T33613.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Claim 14; Page 48; 113pp; English.
CC Splice variants (W00726-28) of the human vascular endothelial growth
CC factor-like polypeptide SOM175 (see also W00725) are products of
CC CDNA clones (see also T33611-13) respectively lacking exon 6, exons
CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at
CC least 1 of the properties of SOM175 including the ability to induce
CC proliferation of vascular endothelial cells, to interact with
CC flt-1/flk-1 receptors, and to induce cell migration, cell survival
CC and/or an increase in intracellular levels of alkaline phosphatase.
CC Recombinant SOM175 proteins can be used to induce astroglial
CC proliferation and to promote neural survival and/or proliferation.
SQ Sequence 101 AA;

Query Match 37.6%; Score 83; DB 19; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.21e-121;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 18 pagavsqdapgqhrkvsvdytracqprevvplvtelmgvtakqlpvcstvtgr 77
AC W04824;
DT 28-APR-1997 (first entry)
DE Vascular endothelial growth factor fragment #1.
KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW Vascular permeability factor; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
OS Mus musculus.
PN W09626736-41.
PD 06-SEP-1996.
PF 01-MAR-1996; 002957.
PR 01-MAR-1995; US-397651.
PR 06-JUN-1995; US-469427.
PR 06-DEC-1995; US-569063.
PA (LUDM-) LUDMIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
PI WPI: 96-412582/41.
DR N-PSDB: T37909.
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
PS Claim 18; Page 53-54; 107pp; English.
CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which it
CC is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting endothelial
CC cell growth during normal embryonic development, wound healing, and

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CC tissue regeneration/reorganisation. The VEGF proteins of the invention
CC share the angiogenic and other properties of VEGF, but are distributed
CC and expressed in tissues differently to VEGF. The proteins can therefore
CC be used to accelerate angiogenesis in wound healing. Antibodies against
CC the proteins can be used for inhibiting angiogenesis. The antibodies can
CC also be used diagnostically to quantitatively detect VEGF-B. Primers
CC complementary to the coding sequences for the proteins of the invention
CC can also be used to detect VEGF-B coding sequences. Quantification of
CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
CC metastatic risk. VEGF-B expression in a cell can be retarded using
CC antisense sequences direct against the VEGF coding sequences, this is
CC especially useful in retarding VEGF expression in tumour cells.
SQ Sequence 102 AA.

Query Match 17.6%; Score 39; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.35e-48;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 kqlvpsctvgrcgccpddglaecvptgqhyrmlm1 73
Oy 65 kqlvpsctvgrcgccpddglaecvptgqhyrmlm1 103

RESULT 9
ID W04828 standard; Protein; 133 AA.

AC W04828:
DE 28-APR-1997 (first entry)
KW Vascular endothelial growth factor-B112.
KW VEGF; endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW VEGF; endothelial cell; proliferation; cell mitogen; angiogenesis; cell growth;
KW embryonic development; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
OS Mus musculus.

PN W09626736-A1.
PD 06-SEP-1996.
PF 01-MAR-1996; U02957.
PR 01-MAR-1995; US-397651.
PR 06-JUN-1995; US-469427.
PR 06-DEC-1995; US-569063.
PA (LUDWIG) LUDWIG INST CANCER RES.
PA (UHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
DR WPI: 96-412582/41.
DR N-PSDB: T37912.

PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
PS Clam 18; Page 58; 107pp; English.
CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which it
CC is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting endothelial
CC cell growth during normal embryonic development, wound healing, and
CC tissue regeneration/reorganisation. The VEGF proteins of the invention
CC share the angiogenic and other properties of VEGF, but are distributed
CC and expressed in tissues differently to VEGF. The proteins can therefore
CC be used to accelerate angiogenesis in wound healing. Antibodies against
CC the proteins can be used for inhibiting angiogenesis. The antibodies can
CC also be used diagnostically to quantitatively detect VEGF-B. Primers
CC complementary to the coding sequences for the proteins of the invention
CC can also be used to detect VEGF-B coding sequences. Quantification of
CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
CC metastatic risk. VEGF-B expression in a cell can be retarded using
CC antisense sequences direct against the VEGF coding sequences, this is
CC especially useful in retarding VEGF expression in tumour cells.
SQ Sequence 133 AA.

Query Match 17.6%; Score 39; DB 21; Length 133;
Best Local Similarity 100.0%; Pred. No. 4.35e-48;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 66 kqlvpsctvgrcgccpddglaecvptgqhyrmlm1 104
Oy 65 kqlvpsctvgrcgccpddglaecvptgqhyrmlm1 103

RESULT 10
ID W04826 standard; Protein; 188 AA.

AC W04826:
DE 28-APR-1997 (first entry)
KW Heart vascular endothelial growth factor-B167.
KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
KW VEGF; endothelial cell; proliferation; cell mitogen; angiogenesis; cell growth;
KW VEGF; endothelial cell; proliferation; wound healing; tissue reorganisation; antibody;
KW cancer; metastatic risk; tumour cell; mouse.
OS Mus musculus.

PN W09626736-A1.
PD 06-SEP-1996.
PF 01-MAR-1996; U02957.
PR 01-MAR-1995; US-397651.
PR 06-JUN-1995; US-469427.
PR 06-DEC-1995; US-569063.
PA (LUDWIG) LUDWIG INST CANCER RES.
PA (UHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
DR WPI: 96-412582/41.
DR N-PSDB: T37910.

PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
PS Clam 18; Page 55-56; 107pp; English.
CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
CC proteins of the invention, which promote endothelial or mesodermal cell
CC proliferation. VEGF is also a glycosylated cationic dimer, and is
CC sometimes referred to as vascular permeability factor (VPF). VEGF has
CC diverse effects, depending on the specific biological context in which it
CC is found. VEGF is a potent endothelial cell mitogen, and directly
CC contributes to induction of angiogenesis in vivo by promoting endothelial
CC cell growth during normal embryonic development, wound healing, and
CC tissue regeneration/reorganisation. The VEGF proteins of the invention
CC share the angiogenic and other properties of VEGF, but are distributed
CC and expressed in tissues differently to VEGF. The proteins can therefore
CC be used to accelerate angiogenesis in wound healing. Antibodies against
CC the proteins can be used for inhibiting angiogenesis. The antibodies can
CC also be used diagnostically to quantitatively detect VEGF-B. Primers
CC complementary to the coding sequences for the proteins of the invention
CC can also be used to detect VEGF-B coding sequences. Quantification of
CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
CC metastatic risk. VEGF-B expression in a cell can be retarded using
CC antisense sequences direct against the VEGF coding sequences, this is
CC especially useful in retarding VEGF expression in tumour cells.
SQ Sequence 188 AA.

Query Match 17.6%; Score 39; DB 21; Length 188;
Best Local Similarity 100.0%; Pred. No. 4.35e-48;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 66 kqlvpsctvgrcgccpddglaecvptgqhyrmlm1 104
Oy 65 kqlvpsctvgrcgccpddglaecvptgqhyrmlm1 103

RESULT 11
ID W00864 standard; Protein; 188 AA.

AC W00864:
DE 30-NOV-1996 (first entry)
KW Murine VRF167.
KW VRF; vascular endothelial growth factor; VEGF; SOM175; neuron;
KW astroglial proliferation.
OS Mus musculus.
FH Key Location/Qualifiers

FT peptide 1..21
 /label= sig-peptide
 PN W0627007-A1.
 PE 06-SEP-1996.
 PR 22-FEB-1996: AU0094.
 PR 02-MAR-1995: AU-001457.
 PR 20-NOV-1995: AU-006647.
 PR 22-DEC-1995: AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M.
 PI Weber G.
 DR WPI: 96-412774/41.
 DR N-PSDB: T13810.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival
 PS Example 5: Fig 9: 113pp; English.
 CC VRF167 (W00863) is the murine homologue of an alternatively spliced
 CC variant (W00726) of human vascular endothelial growth factor-like
 CC polypeptide SOM175 (W00725), a protein capable of inducing astroglial
 CC proliferation and of promoting neural survival and/or proliferation.
 CC Its amino acid sequence was deduced from a cDNA clone (T13810)
 CC isolated from a new-born mouse brain cDNA library. VRF167 shows
 CC 88% identity and 92% similarity to its human counterpart. It lacks
 CC 101 amino acids found in VRF186 (W00863), the murine homologue
 CC of SOM175, owing to a deletion of exon 6 during splicing.
 SQ Sequence 188 AA;

Query Match 17.6%; Score 39; DB 19; Length 188;
 Best Local Similarity 100.0%; Pred. No. 4.35e-48;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 66 kqlvpvcvtvrgcgccpddgldcvtptqhvrmqjlm1 104
 ||||||||||||||||||||||||||||||||||||||||
 QY 65 kqlvpvcvtvrgcgccpddgldcvtptqhvrmqjlm1 103

RESULT 12
 ID W04830 standard; Protein; 207 AA.
 AC W04830:
 DT 28-APR-1997 (first entry)
 DE Vascular endothelial growth factor-B186.
 KW Vascular endothelial cell; proliferation; vascular endothelial growth factor; VPF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse.
 OS Mus musculus.
 PN W09626736-A1.
 PD 06-SEP-1996.
 PE 01-MAR-1996: U02957.
 PR 01-NOV-1995: US-307651.
 PR 06-JUN-1995: US-469427.
 PR 06-DEC-1995: US-569063.
 PA (LUDWIG) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 PI Allitalo K, Eriksson U, Olofsson B, Pajusola K.
 DR WPI: 96-412582/41.
 DR N-PSDB: T37914.
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis
 PS Claim 18: Page 60-61: 107pp; English.
 CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
 CC proteins of the invention, which promote endothelial or mesodermal cell
 CC proliferation. VEGF is also a glycosylated cationic dimer, and is
 CC sometimes referred to as vascular permeability factor (VPF). VEGF has
 CC diverse effects, depending on the specific biological context in which it
 CC is found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting endothelial
 CC cell growth during normal embryonic development, wound healing, and
 CC tissue regeneration/reorganisation. The VEGF proteins of the invention
 CC share the angiogenic and other properties of VEGF, but are distributed

CC and expressed in tissues differently to VEGF. The proteins can therefore
 CC be used to accelerate angiogenesis in wound healing. Antibodies against
 CC the proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences directed against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.
 SQ Sequence 207 AA;

Query Match 17.6%; Score 39; DB 21; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.35e-48;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 66 kqlvpvcvtvrgcgccpddgldcvtptqhvrmqjlm1 104
 ||||||||||||||||||||||||||||||||||||||||
 QY 65 kqlvpvcvtvrgcgccpddgldcvtptqhvrmqjlm1 103

RESULT 13
 ID W00863 standard; Protein; 207 AA.
 AC W00863:
 DT 30-NOV-1996 (first entry)
 DE Murine VRF186.
 KW VRF: vascular endothelial growth factor; VEGF; SOM175; neuron;
 KW astroglial proliferation.
 OS Mus musculus.
 FH Key
 FT peptide 1..21
 /label= sig-peptide
 PN W09627007-A1.
 PD 06-SEP-1996.
 PE 22-FEB-1996: AU0094.
 PR 02-MAR-1995: AU-001457.
 PR 20-NOV-1995: AU-006647.
 PR 22-DEC-1995: AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M.
 PI Weber G.
 DR WPI: 96-412774/41.
 DR N-PSDB: T13809.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival
 PS Example 5: Fig 9: 113pp; English.
 CC VRF186 (W00863) is the murine homologue of human vascular endothelial
 CC growth factor-like polypeptide SOM175 (W00725), a protein capable of
 CC inducing astroglial proliferation and of promoting neural survival
 CC and/or proliferation. Its amino acid sequence was deduced from a
 CC cDNA clone (T13809) isolated from a new-born mouse brain cDNA
 CC library. An alternatively spliced variant, VRF169 (W00864), was
 CC also identified.
 SQ Sequence 207 AA;

Query Match 17.6%; Score 39; DB 19; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.35e-48;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 66 kqlvpvcvtvrgcgccpddgldcvtptqhvrmqjlm1 104
 ||||||||||||||||||||||||||||||||||||||||
 QY 65 kqlvpvcvtvrgcgccpddgldcvtptqhvrmqjlm1 103

RESULT 14
 ID W04827 standard; Protein; 195 AA.
 AC W04827:
 DT 28-APR-1997 (first entry)
 DE Heart vascular endothelial growth factor-B174.
 KW Vascular endothelial cell; proliferation; vascular endothelial growth factor; VPF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;

KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse.
 OS Mus musculus.
 PN W04824-W04831.
 PD 06-SEP-1996.
 PF 01-MAR-1996; U02957.
 PR 01-MAR-1995; US-397651.
 PR 06-JUN-1995; US-469427.
 PR 06-DEC-1995; US-569063.
 PA (LUDM-) LUDMIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
 PI WPI: 96-412582/41.
 DR N-PSDB: 137911.
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing; also related nucleic acid
 PT and antibodies for cancer diagnosis.
 PS Claim 18; Page 56-57; 107pp; English.
 CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
 CC proteins of the invention, which promote endothelial or mesodermal cell
 CC proliferation. VEGF is also a glycosylated cationic dimer, and is
 CC sometimes referred to as vascular permeability factor (VPF). VEGF has
 CC diverse effects, depending on the specific biological context in which it
 CC is found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting endothelial
 CC cell growth during normal embryonic development, wound healing, and
 CC tissue regeneration/reorganisation. The VEGF proteins of the invention
 CC share the angiogenic and other properties of VEGF, but are distributed
 CC and expressed in tissues differently to VEGF. The proteins can therefore
 CC be used to accelerate angiogenesis in wound healing. Antibodies against
 CC the proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences direct against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.
 SQ Sequence 195 AA;

Query Match 15.8%; Score 35; DB 21; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.32e-41;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 66 KGLVPSCVTVRCGCGCCPDGGLCVPTGQHVYRMQ 100
 |||
 QY 65 KGLVPSCVTVRCGCGCCPDGGLCVPTGQHVYRMQ 99

RESULT 15
 ID W04833 standard; peptide: 23 AA.
 AC W04833.
 DT 30-APR-1997 (first entry)
 DE N-terminal peptide of vascular endothelial growth factor-B.
 KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; human.
 OS Homo sapiens.
 PN W09626736-A1.
 PD 06-SEP-1996.
 PF 01-MAR-1996; U02957.
 PR 01-MAR-1995; US-397651.
 PR 06-JUN-1995; US-469427.
 PR 06-DEC-1995; US-569063.
 PA (LUDM-) LUDMIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
 PI WPI: 96-412582/41.
 DR Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing; also related nucleic acid
 PT and antibodies for cancer diagnosis

PS Example 8; Page 31; 107pp; English.
 CC This sequence represents the N-terminal peptide of a vascular endothelial
 CC growth factor (VEGF) protein of the invention (see W04824-W04831). This
 CC sequence was coupled to keyhole limpet haemocyanin, to produce antibodies
 CC against human VEGF-B. VEGF is a glycosylated cationic dimer, which
 CC promotes endothelial or mesodermal cell proliferation, and is sometimes
 CC referred to as vascular permeability factor (VPF). VEGF has diverse
 CC effects, depending on the specific biological context in which it is
 CC found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting endothelial
 CC cell growth during normal embryonic development, wound healing, and
 CC tissue regeneration/reorganisation. The VEGF proteins of the invention
 CC share the angiogenic and other properties of VEGF, but are distributed
 CC and expressed in tissues differently to VEGF. The proteins can therefore
 CC be used to accelerate angiogenesis in wound healing. Antibodies against
 CC the proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences direct against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.
 SQ Sequence 23 AA;

Query Match 10.4%; Score 23; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.47e-22;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 sgpdapghrkxvswldtyrtat 23
 |||
 QY 23 SQPDAPGHQRKXVSWIDYTRAT 45

Search completed: Mon Nov 30 13:09:07 1998
 Job time : 50 secs.

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Nov 26 00:01:57 1998: Maspar time 4.69 Seconds

Tabular output not generated. 148,639 Million cell updates/sec

Title: >US-09-033-662-2
Description: (69-82) from US09033662.pep
Perfect Score: 121
Sequence: 1 PSCVTYQRCGGCCP 14

Scoring table:
PAM 150
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl6
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 23.748: Variance 38.778: scale 0.612

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	121	100.0	116	11	035485	VASCULAR ENDOTHELIAL G 1.08e-12
2	121	100.0	150	11	054881	VASCULAR ENDOTHELIAL G 1.08e-12
3	121	100.0	207	11	064290	VASCULAR ENDOTHELIAL G 1.08e-12
4	121	100.0	207	4	016528	VEGF RELATED FACTOR IS 1.08e-12
5	97	80.2	183	11	063740	PDGF PROTEIN (FRAGMENT 1.38e-07
6	97	80.2	185	4	015354	C-SIS ONCOGENE (PLATEL 1.38e-07
7	97	80.2	210	6	029613	C-SIS ONCOGENE (PLATEL 1.38e-07
8	97	80.2	271	14	041283	POLYPROTEIN PRECURSOR 1.38e-07
9	93	76.9	232	4	016889	VASCULAR ENDOTHELIAL G 9.15e-07
10	92	76.0	418	13	057352	VASCULAR ENDOTHELIAL G 1.46e-06
11	91	75.2	75	6	018843	VASCULAR ENDOTHELIAL G 2.34e-06
12	91	75.2	326	11	035251	VASCULAR ENDOTHELIAL G 2.34e-06
13	91	75.2	354	4	043915	GROWTH FACTOR FIGF. 2.34e-06
14	91	75.2	358	11	P97946	VASCULAR ENDOTHELIAL G 2.34e-06
15	87	71.9	141	11	070123	VEGF115. 1.49e-05
16	87	71.9	144	13	073822	VASCULAR ENDOTHELIAL G 1.49e-05
17	87	71.9	148	13	042571	VASCULAR ENDOTHELIAL G 1.49e-05
18	87	71.9	188	13	073682	VASCULAR ENDOTHELIAL G 1.49e-05
19	87	71.9	194	13	042572	VASCULAR ENDOTHELIAL G 1.49e-05
20	84	69.4	158	11	063434	PLACENTA GROWTH FACTOR 5.89e-05

21	75	62.0	463	2	007346	PMCA, COMPLETE CDS. 3.27e-03
22	75	62.0	463	2	P73374	HYPOTHETICAL 51.5 KD P 3.27e-03
23	72	59.5	126	11	035757	VASCULAR ENDOTHELIAL G 1.20e-03
24	64	52.9	476	14	080890	ENNAL. 3.45e-01
25	64	52.9	2168	14	041174	POLYPROTEIN. 3.45e-01
26	62	51.2	1017	5	060960	L3162-112. 7.75e-01
27	62	51.2	1017	5	060960	7.75e-01
28	61	50.4	327	5	023258	SIMILAR TO CUTICLE COL 1.16e+00
29	61	50.4	327	5	018975	1.16e+00
30	59	48.8	466	2	031545	F10D2.3 PROTEIN. 1.16e+00
31	58	47.9	2225	5	045881	VEFO PROTEIN. 3.77e+00
32	57	47.1	159	10	065372	W01F3.3. 3.77e+00
33	57	47.1	168	13	090653	F1F1.6. 5.54e+00
34	57	47.1	175	4	007628	CELL DIVISION CYCLE CO 5.54e+00
35	57	47.1	177	4	007627	KERATIN, HIGH-SULFUR M 5.54e+00
36	57	47.1	1361	14	086623	KERATIN, HIGH-SULFUR M 5.54e+00
37	57	47.1	1361	14	086623	SURFACE GLYCOPROTEIN S 5.54e+00
38	57	47.1	1361	14	086623	SURFACE PROTEIN PRECUR 5.54e+00
39	57	47.1	1361	14	086623	SURFACE PROTEIN PRECUR 5.54e+00
40	56	46.3	375	2	068393	FK506 POLYMERIDE SYNTH 5.54e+00
41	56	46.3	511	1	029309	RADICAL ACTIVATING PRO 8.13e+00
42	55	45.5	108	2	005928	GLUTAMATE SYNTHASE (GL 1.19e+01
43	55	45.5	133	2	006787	PURATIVE TRANSCRIPTION 1.19e+01
44	55	45.5	286	5	044160	HYPOTHETICAL 12.7 KD P 1.19e+01
45	55	45.5	4114	11	054796	CD4.2 PROTEIN. 1.19e+01
						TENASCIN-X. 1.19e+01

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	116 AA.
ID 035485;			
AC 035485;			
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B 186 PRECURSOR (FRAGMENT).			
OS RATTUS NORVEGICUS (RAT).			
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC EUTHERIA; RODENTIA.			
NC [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-PLACENTA;			
RA MANDRIOTA S.J.; PEPPER M.S.;			
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR EMBL: AF032925; G2641622; -			
DR PROSITE: PS00249; PDGF. 1.			
DR PFM; PF00341; PDGF.			
FT NON_TER 1			
FT NON_TER 116			
SO SEQUENCE 116 AA; 12743 MW; 106E2733 CRC32;			
Query Match 100.0%; Score 121; DB 11; Length 116;			
Best Local Similarity 100.0%; Pred. No. 1.08e-12;			
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DB 20 PSCVTYQRCGGCCP 33			
QY 69 PSCVTYQRCGGCCP 82			
RESULT 2	PRELIMINARY:	PRT:	150 AA.
ID 054881;			
AC 054881;			
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)			
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)			
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)			
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B (FRAGMENT).			
OS RATTUS NORVEGICUS (RAT).			
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC EUTHERIA; RODENTIA.			
NC [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE-HEART;			

RA WEIL J., ESCHENHAGEN T., MITTMANN C., SCHOLZ H.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF022952; G276602;
 DR PROSITE: PS00249; PDGF; 1.
 FT NON-TER 1
 FT NON-TER 150
 SO SEQUENCE 150 AA; 17243 MW; D088D4D3 CRC32;

Query Match 100.0%; Score 121; DB 11; Length 150;
 Best Local Similarity 100.0%; Pred. No. 1,08e-12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 PSCVTYORCGGCCP 52
 OY 69 PSCVTYORCGGCCP 82

RESULT 3
 ID 064290; PRELIMINARY; PRT; 207 AA.
 AC 064290;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN
 DE (VASCULAR ENDOTHELIAL GROWTH FACTOR B 186).
 GN VRF OR VEGF-B.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HEART;
 RX MEDLINE: 96197355.
 RA OLOFSSON B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HEART;
 RX MEDLINE: 96325041.
 RA OLOFSSON B.; PAUSOLA K., VON EULER G., CHILOV D., ALLTALO K.,
 RA ERIKSSON U.;
 RL J. BIOL. CHEM. 271:19310-19317(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-WHOLE BRAIN;
 RX MEDLINE: 96183052.
 RA TOWNSON S., LAGERCRANTZ J., GRIMOND S., STILINS G., NORDENSKJOLD M.,
 RA WEBER G., HAYWARD N.K.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 220:922-928(1996).
 DR EMBL: U52820; G1488261;
 DR EMBL: U43836; G1314334;
 DR MGD; MGI:106199; VRF;
 DR PROSITE: PS00249; PDGF; 1.
 DR PFAM: PF00341; PDGF.
 SO SEQUENCE 207 AA; 21914 MW; 4FB6C405 CRC32;

Query Match 100.0%; Score 121; DB 11; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1,08e-12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 PSCVTYORCGGCCP 83
 OY 69 PSCVTYORCGGCCP 82

RESULT 4
 ID 016528; PRELIMINARY; PRT; 207 AA.
 AC 016528;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR,
 GN VRF OR VEGF-B.

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA GRIMOND S., LAGERCRANTZ J., DRINKWATER C., STILINS G., TOWNSON S.,
 RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L.,
 RA HAYWARD N., WEBER G.;
 RL GENOME RES. 6:122-129(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FIBROSARCOMA HT-1080;
 RX MEDLINE: 96197355.
 RA OLOFSSON B.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FIBROSARCOMA HT-1080;
 RX MEDLINE: 96197355.
 RA OLOFSSON B.;
 RL J. BIOL. CHEM. 271:19310-19317(1996).
 DR EMBL: U43368; G1216396;
 DR PROSITE: PS00249; PDGF; 1.
 DR PFAM: PF00341; PDGF.
 KM SIGNAL.
 FT CHAIN 1
 FT SIGNAL 21
 FT CHAIN 22
 SO SEQUENCE 207 AA; 21602 MW; 16BDF6F1 CRC32;

Query Match 100.0%; Score 121; DB 4; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1,08e-12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 PSCVTYORCGGCCP 83
 OY 69 PSCVTYORCGGCCP 82

RESULT 5
 ID 063740; PRELIMINARY; PRT; 183 AA.
 AC 063740;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE PDGF PROTEIN (FRAGMENT).
 GN C-SIS.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RA MOATS-STRAUS B.M., XU L., JARVIS W., STILES A.D.;
 RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U41623; G769680;
 DR PROSITE: PS00249; PDGF; 1.
 DR PFAM: PF00341; PDGF.
 FT NON-TER 1
 FT NON-TER 183
 SO SEQUENCE 183 AA; 20160 MW; 69908655 CRC32;

Query Match 80.2%; Score 97; DB 11; Length 183;
 Best Local Similarity 76.9%; Pred. No. 1.38e-07;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 104 PSCVTYORCGGCC 116
 OY 69 PSCVTYORCGGCC 81

RESULT	6	PRELIMINARY:	PR:	165 AA.
ID	015354			
AC	015354:			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	C-SIS PROTO-ONCOGENE (FRAGMENT).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUHAROTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUHAROTA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=CHORIOCARCINOMA;			
RX	MEDLINE; 95388493.			
RA	DIRKS R.P.H., ONNEKINK C., JANSSEN H.J., DE JONG A., BLOEMERS H.P.J.;			
RL	NUCLEIC ACIDS RES. 23:2815-2822(1995).			
DR	EMBL; X83705; G951025; -			
DR	PROSITE; PS00249; PDGF; 1.			
DR	PFAM; PF00341; PDGF.			
FT	NON_TER 185			
SO	SEQUENCE 185 AA; 20774 MW; C5FAA883 CRC32;			
Query Match	80.2%;	Score 97;	DB 6;	Length 185;
Best Local Similarity	76.9%;	Pred. No. 1.38e-07;		
Matches	10; Conservative	2; Mismatches	1; Indels	0; Gaps
Db	107 PCCEVQRCGCC 119			
Oy	69 PSCVTYQRCGCC 81			
RESULT	7	PRELIMINARY:	PR:	210 AA.
ID	Q29613			
AC	Q29613:			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	C-SIS ONCOGENE (PLATELET-DERIVED GROWTH FACTOR).			
OS	FELIS SILVESTRIIS CATUS (CAT).			
OC	EUHAROTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUHAROTA; CARNIVORA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 8716463.			
RA	VAN DEN OMELAND A.M.M., VAN GRONINGEN J.J.M., SCHALKEN J.A.;			
RA	VAN NECK H.W., BLOEMERS P.J., VAN DE VEN W.J.M.;			
RL	NUCLEIC ACIDS RES. 15:959-970(1987).			
RN	[2]			
RP	SEQUENCE OF 1-21 FROM N.A.			
RX	MEDLINE; 86120370.			
RA	VAN DEN OMELAND A.M.M., ROEBROEK A.J.M., SCHALKEN J.A.;			
RA	CLAESSEN C.A.A., BLOEMERS H.P.J., VAN DE VEN W.J.M.;			
RL	NUCLEIC ACIDS RES. 14:765-778(1986).			
DR	EMBL; X06297; E222210; -			
DR	EMBL; X06298; E222210; JOINED.			
DR	EMBL; X06299; E222210; JOINED.			
DR	EMBL; X06300; E222210; JOINED.			
DR	EMBL; X06301; E222210; JOINED.			
DR	EMBL; X06302; E222210; JOINED.			
DR	EMBL; X03494; G1110; -			
DR	EMBL; M25358; G163887; -			
DR	EMBL; M25359; G163887; JOINED.			
DR	EMBL; M25354; G163887; JOINED.			
DR	EMBL; M25355; G163887; JOINED.			
DR	EMBL; M25356; G163887; JOINED.			
DR	EMBL; M25357; G163887; JOINED.			
DR	PROSITE; PS00249; PDGF; 1.			
DR	PFAM; PF00341; PDGF.			
SO	SEQUENCE 210 AA; 23649 MW; 1579ED72 CRC32;			
Query Match	80.2%;	Score 97;	DB 6;	Length 210;
Best Local Similarity	76.9%;	Pred. No. 1.38e-07;		
Matches	10; Conservative	2; Mismatches	1; Indels	0; Gaps

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Db 126 PRCVYORCGGCC 138
OY 69 PSCVTVORCGGCC 81

RESULT 8
ID 041283 PRELIMINARY; PRT; 271 AA.
AC 041283;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE POLYPROTEIN PRECURSOR ENV-SIS.
OS SIMIAN SARCOMA VIRUS.
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC ONCOVIRINAE.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 83144004.
RA DEVARE S.G., REDDY P.E., LAW J.D., ROBBINS K.C., AARONSON S.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 80:731-735(1983).
DR EMBL: J02394; G32621;
DR PROSITE: PS00249; PDGF; 1.
DR PFAM: PF00341; PDGF.
KM POLYPROTEIN.
SQ SEQUENCE 271 AA; 30328 MW; 17F778D3 CRC32;

Query Match 80.2%; Score 97; DB 14; Length 271;
Best Local Similarity 76.9%; Pred. No. 1.38e-07;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 152 PRCVYORCGGCC 164
OY 69 PSCVTVORCGGCC 81

RESULT 9
ID 016889 PRELIMINARY; PRT; 232 AA.
AC 016889;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 92168017.
RA HOUICK K.A., FERRARA N., WINER J., CACHIANES G., LI B., LEUNG D.W.;
RL MOL. ENDOCRINOL. 5:1806-1814(1991).
DR EMBL: S85192; G246156;
DR EMBL: S85224; E91787;
DR EMBL: S85199; E91787; JOINED.
DR EMBL: S85201; E91787; JOINED.
DR EMBL: S85219; E91787; JOINED.
DR EMBL: S85222; E91787; JOINED.
DR PROSITE: PS00249; PDGF; 1.
DR PFAM: PF00341; PDGF.
SQ SEQUENCE 232 AA; 27042 MW; 344182D1 CRC32;

Query Match 76.9%; Score 93; DB 4; Length 232;
Best Local Similarity 76.9%; Pred. No. 9.15e-07;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 75 PSCVPLMRCGCC 87
OY 69 PSCVTVORCGGCC 81

RESULT 10
ID 057352 PRELIMINARY; PRT; 418 AA.
AC 057352;

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DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
GN VEGF-C.
OS COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RA EICHMANN A., CORBEL C., JAFFREDO T., BREANT V., JOUKOV V., KUMAR V.,
RA ALITALO K., LE DOUARIN N.M.;
RL DEVELOPMENT 125:743-752(1998).
DR EMBL: Y15837, E1215492; -.
DR PROSITE: PS00249; PDGF. 1.
KW SIGNAL.
FT CHAIN 111 418 POTENTIAL.
SQ SEQUENCE 418 AA; 46839 MW; B7862854 CRC32;

Query Match
Best Local Similarity 76.0%; Score 92; DB 13; Length 418;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 153 PSCVTVQRCGCC 165
QY 69 PSCVTVQRCGCC 81

RESULT 11
ID 018843; PRELIMINARY; PRT; 75 AA.
AC 018843;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR (FRAGMENT).
GN VEGF.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; LAGOMORPHA.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WHITE NEW ZEALAND; TISSUE-SKELETAL MUSCLE;
RC MEDLINE: 96191144.
RA SKORJANC D., JASCHINSKI F., HEINE G., PETTE D.;
RL AM. J. PHYSIOL. 274:0-0(1998).
DR EMBL: AF022179; G2465453; -.
DR PROSITE: PS00249; PDGF. 1.
DR PFAM: PF00341; PDGF. 1.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8720 MW; 716988DE CRC32;

Query Match
Best Local Similarity 75.2%; Score 91; DB 6; Length 75;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 17 PSCVTVQRCGCC 29
QY 69 PSCVTVQRCGCC 81

RESULT 12
ID 035251; PRELIMINARY; PRT; 326 AA.
AC 035251;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR D.
GN VEGF-D.
OS RATUUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY;
RX MEDLINE: 97349118.
RA YAMADA Y., NEZU J., SHIMANE M., HIRATA Y.;
RL GENOMICS 42:483-488(1997).
DR EMBL: AF014827; G2323339; -.
DR PROSITE: PS00249; PDGF. 1.
DR PFAM: PF00341; PDGF. 1.
SQ SEQUENCE 326 AA; 37112 MW; B30608D3 CRC32;

Query Match
Best Local Similarity 75.9%; Score 91; DB 11; Length 326;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 139 PSCVTVQRCGCC 151
QY 69 PSCVTVQRCGCC 81

RESULT 13
ID 043915; PRELIMINARY; PRT; 354 AA.
AC 043915;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE GROWTH FACTOR FIGF.
GN FIGF OR VEGF-D.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ROCCHIGIANI M., LESTINGI M., LUDDI A., ORLANDINI M., FRANCO B.,
RA ROSSI E., BALABBO A., ZUFFARDI O., OLIVIERO S.;
RL GENOMICS 47:207-216(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA YAMADA Y., NEZU J., SHIMANE M., HIRATA Y.;
RL GENOMICS 42:483-488(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA ACHEN M.G., JELTSCH M., KUKK E., MAERINEN T., VITALI A., WILKS A.F.,
RA ALITALO K., STACKER S.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 95:548-553(1998).
DR EMBL: Y12864; E1252372; -.
DR EMBL: Y12865; E1252372; JOINED.
DR EMBL: Y12866; E1252372; JOINED.
DR EMBL: Y12867; E1252372; JOINED.
DR EMBL: Y12868; E1252372; JOINED.
DR EMBL: Y12869; E1252372; JOINED.
DR EMBL: Y12870; E1252372; JOINED.
DR EMBL: D89630; E1025175; -.
DR EMBL: AJ000185; E1250855; -.
DR EMBL: Y12863; E1252270; -.
DR PROSITE: PS00249; PDGF. 1.
SQ SEQUENCE 354 AA; 40444 MW; 310D8150 CRC32;

Query Match
Best Local Similarity 75.2%; Score 91; DB 4; Length 354;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 134 PSCVTVQRCGCC 146
QY 69 PSCVTVQRCGCC 81

RESULT 14
ID P97946; PRELIMINARY; PRT; 358 AA.
AC P97946;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)

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DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR D (C-FOS INDUCED GROWTH FACTOR).
 GN VEGF-D OR FIGF.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J;
 RA ORDANDINI M., MARCONCINI L., FERRUZZI R., OLIVIERO S.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:11675-11675(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RX MEDLINE: 97349118.
 RA YAMADA Y., NEZU J., SHIMANE M., HIRATA Y.;
 RL GENOMICS 42:483-488(1997).
 DR EMBL: X89572; E283242; -;
 DR EMBL: D89628; D1014701; -;
 DR MGD: MGI:108037; FIGF.
 DR PROSITE: PS00249; PDGF; 1.
 DR PFAM: PF00341; PDGF.
 SO SEQUENCE 358 AA; 40908 MW; 64EB4E9 CRC32;

Query Match 75.28; Score 91; DB 11; Length 358;
 Best Local Similarity 76.98; Pred. No. 2.34e-06;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 139 PSCVNWRCGGCC 151
 QY 69 PSCVTWORCGGCC 81

RESULT 15
 ID 070123 PRELIMINARY; PRT; 141 AA.
 AC 070123;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE VEGF15.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ICR;
 RX MEDLINE: 95101726.
 RA SUGIHARA T., KAUL S.C., MITSUI Y., MADHWA R.;
 RL BIOCHIM. BIOPHYS. ACTA 1224:365-370(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ICR;
 RX MEDLINE: 98112857.
 RA SUGIHARA T., MADHWA R., KAUL S.C., MITSUI Y.;
 RL J. BIOL. CHEM. 273:3033-3038(1998).
 DR EMBL: U50279; G2951983; -;
 DR PROSITE: PS00249; PDGF; 1.
 SO SEQUENCE 141 AA; 15550 MW; 774CB7D2 CRC32;

Query Match 71.98; Score 87; DB 11; Length 141;
 Best Local Similarity 69.28; Pred. No. 1.49e-05;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 74 PSCVPLMRCAGCC 86
 QY 69 PSCVTWORCGGCC 81

Search completed: Thu Nov 26 00:02:49 1998
 Job time : 52 secs.

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QY 69 PSCVTYVQRCGCCP 82

RESULT 2

ID VEGF_MOUSE STANDARD: PRT: 188 AA.

AC P49766:

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR

DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).

OS VEGF OR VRF.

GN MUS MUSCULUS (MOUSE)

OC EUKARYOTA; MEIZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART;

RX MEDLINE: 96197355

RA CLORESSON B., PAJUSOLA K., KAIPIAINEN A., VON EULER G., JOUKOV V.,

RA SAKSELA O., ORPANA A., PETERSSON R.F., ALITALO K., ERIKSSON U.,

RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RX MEDLINE: 96183052

RA TOWNSON S., LAGERCRANTZ J., GRIMMOND S., SILINS G.,

RA NORRENSKJOLD M., WEBER G., HAYWARD N.K.;

RL BIOCHEM. BIOPHYS. RES. COMMUN. 220:922-928(1996).

CC -1- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.

CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER

CC WITH VEGF.

CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR

CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.

CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY

CC AND SKELETAL MUSCLE.

CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

DR EMBL: U48800; G1234825; -

DR EMBL: U43837; G1314336; -

DR MGD: MG1:106199; VRF.

DR PROSITE: PS00249; PDGF: 1.

KW MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.

FT SIGNAL

FT CHAIN 1 21 POTENTIAL.

FT SEQUENCE 188 AA; 21442 MW; 7999A3C8 CRC32;

Query Match 100.0%; Score 121; DB 1; Length 188;

Best Local Similarity 100.0%; Pred. No. 5.15e-13;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 70 PSCVTYVQRCGCCP 83

QY 69 PSCVTYVQRCGCCP 82

RESULT 3

ID PDGF_RAT STANDARD: PRT: 225 AA.

AC Q05028:

DT 01-FEB-1994 (REL. 28, CREATED)

DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)

DE (PDGF-2) (FRAGMENT).

OS PDGFB.

GN RATRUS NORVEGICUS (RAT)

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE: 93305723.

RA HEHREN B., MEYER K.A., ROUGE M., LOETSCHER P., PECH M.;

RL BIOCHIM. BIOPHYS. ACTA 1173:294-302(1993).

RN [2]

RP SEQUENCE OF 74-182 FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY; TISSUE-SMOOTH MUSCLE;

RX MEDLINE: 95277908

RA LINDNER V., GIACHELLI C.M., SCHWARTZ S.M., REIDY M.A.;

RL CIRC. RES. 76:951-957(1995).

CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR

CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS

CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS

CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE

CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.

CC MAY HAVE A CHEMOTACTIC ROLE IN INITIAL THICKENING.

CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A

CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN

CC TRANSFORMATION PROCESSES.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN A DISTINCT SUBPOPULATION

CC OF SMOOTH MUSCLE CELLS IN INJURED ARTERIES.

CC -1- A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.

CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

DR EMBL: 214117; G56868; -

DR EMBL: L40991; G727178; -

DR PIR: S25097; S25097.

DR HSP: P01127; 1PDG.

DR PROSITE: PS00249; PDGF: 1.

KW MITOGEN; GROWTH FACTOR; PROTO-ONCOGENE; PLATELET; SIGNAL.

FT NON_TER 1 1

FT SIGNAL <1 12

FT PROPEP 13 73

FT CHAIN 74 182

FT PROPEP 183 225

FT SITE 100 100

FT SITE 103 103

FT DISULFID 89 133

FT DISULFID 122 170

FT DISULFID 126 172

FT DISULFID 116 116

FT DISULFID 125 125

FT CARBOHYD 55 55

FT NON_TER 225 225

FT SEQUENCE 225 AA; 25603 MW; CC1B043F CRC32;

Query Match 80.2%; Score 97; DB 1; Length 225;

Best Local Similarity 76.9%; Pred. No. 7.65e-08;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 114 PCVEYVQRCGCC 126

QY 69 PSCVTYVQRCGCC 81

RESULT 4

ID TSIS SMSAV STANDARD: PRT: 226 AA.

AC P01128:

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE PDGF-RELATED TRANSFORMING PROTEIN P28-SIS.

GN V-SIS.

OS SIMIAN SARCOMA VIRUS.

OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;

OC ONCOVIRINAE.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 83144004.

RA DEYARE S.G., REDDY E.P., LAW J.D., ROBBINS K.C., AARONSON S.A.;

RL PROC. NATL. ACAD. SCI. U.S.A. 80:731-735(1983).

CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

DR EMBL: V01201; G61777; ALT_INT.

DR PIR: A01381; TWMVS.

DR HSP: P01127; 1PDG.

DR PROSITE: PS00249; PDGF: 1.

KW TRANSFORMING PROTEIN; ONCOGENE; GROWTH FACTOR.

FT SEQUENCE 226 AA; 25411 MW; DD3C74C1 CRC32;

CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84250225.
RA JOSEPHS S.F., RAINER L., CLARKE M.F., WESTIN E.H., REITZ M.S.,
RN WONG-STAL F.;
RL SCIENCE 225:636-639(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86205961.
RA RAO C.D., IGARASHI H., CHIU I.-M., ROBBINS K.C., AARONSON S.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:2392-2396(1986).
RN [3]
RP SEQUENCE OF 22-241 FROM N.A.
RX MEDLINE; 84205633.
RA CHIU I.-M., REDDY E.P., GIOVL D., ROBBINS K.C., TRONICK S.R.,
RN AARONSON S.A.;
RL CELL 37:123-129(1984).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85296313.
RA COLLINS T., GINSBURG D., BOSS J.M., ORKIN S.H., POBER J.S.;
RN NATURE 316:748-750(1985).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85269623.
RA RAINER L., JOSEPHS S.F., JARRETT R., REITZ M.S., WONG-STAL F.;
RN NUCLEIC ACIDS RES. 13:5007-5018(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87217119.
RA RAO C.D., IGARASHI H., PECH M.W., ROBBINS K.C., AARONSON S.A.;
RN COLD SPRING HARB. SYMP. QUANT. BIOL. 51:959-966(1986).
RN [7]
RP SEQUENCE FROM N.A.
RA BURGESS J., ODELL C.;
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [8]
RP SEQUENCE OF 26-241 FROM N.A.
RX MEDLINE; 86164981.
RA WEICH H.A., SEBALD W., SCHAIRER H.U., HOPPE J.;
RN FEBS LETT. 198:344-348(1986).
RN [9]
RP SEQUENCE OF 82-110.
RX MEDLINE; 83197379.
RA ANTONIADES H.N., HUNKAPILLER M.W.;
RL SCIENCE 220:963-965(1983).
RN [10]
RP SEQUENCE OF 82-112.
RX MEDLINE; 83244981.
RA WATERFIELD M.D., SCRACE G.T., WHITTLE N., STROOBANT P., JOHNSON A.;
RL NATURE 304:35-39(1983).
RN [11]
RP MUTAGENESIS, IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING.
RX MEDLINE; 92097530.
RA CLEMENTS J.M., BARDEN L.J., BLOXIDGE R.E., CATLIN G., COOK A.L.,
RN CRAIG S., DUDMOND A.H., EDWARDS R.M., FALLON A., GREEN D.R.,
RA HELLEWELL P.G., KIRWIN P.M., NAYEE P.D., RICHARDSON S.J., BROWN D.,
RN CHAMWALA S.B., SNAREY M., WINSLOW D.;
RL EMO J. 10:4113-4120(1991).
RN [12]
RP INTERCHAIN DISULFIDE BONDS.
RX MEDLINE; 92283833.
RA ANDERSSON M., OESTMAN A., BAECTROEM G., HELLMAN U.,
RN GEORGE-NAASCIMENTO C., WESTERMARK B., HELDIN C.-H.;
RL J. BIOL. CHEM. 267:11260-11266(1992).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE; 93010987.
RA OEFNER C., D'ARCY A., WINKLER F.K., EGGMANN B., HOANG M.;
RN EMO J. 11:3921-3926(1992).
CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR

OS FELIS SILVESTRIS CATUS (CAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; CARNIVORA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 87146463.
 RA VAN DEN OWEELAND A.M.W., VAN GRONINGEN J.J.M., SCHALKEN J.A.,
 RA VAN NECK H.W., BLOEMERS H.P.J., VAN DE VEN W.J.M.,
 RL NUCLEIC ACIDS RES. 15:959-970(1987).
 RN [2]
 RP REVISIONS.
 RA VAN DEN OWEELAND A.M.W.;
 RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC -1- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
 CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
 CC TRANSFORMATION PROCESSES.
 CC -1- A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL: X05112; E281569; ALT-SEQ.
 DR HSP; A26402; TVCTSS.
 DR PROSITE; P500249; PDGF: 1.
 KM MITOGEN: GROWTH FACTOR: PROTO-ONCOGENE; PLATELET; SIGNAL.
 FT SIGNAL 1 20
 FT PROPEP 21 81
 FT CHAIN 82 194
 FT PROPEP 195 245
 FT DISULFID 101 145
 FT DISULFID 134 182
 FT DISULFID 138 184
 FT DISULFID 128 128
 FT DISULFID 137 137
 SQ SEQUENCE 245 AA: 27787 MW: AF5645D8 CRC32:
 Query Match 80.2%; Score 97; DB 1; Length 245;
 Best Local Similarity 76.9%; Pred. No. 7.65e-08;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 126 PCVEYVRCGCGC 138
 Qy 69 PSCVTYVRCGCGC 81
 RESULT 9
 ID VEGH_OREN2 STANDARD; PRT; 133 AA.
 AC P52584;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.
 GN A2R.
 OS ORF VIRUS (STRAIN N22).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHORDOPOXYVIRINAE;
 OC PARAPOXYVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 94076465.
 RA LITTLE D.J., FRASER K.M., FLEMING S.B., MERCER A.A., ROBINSON A.J.;
 RL J. VIROL. 68:84-92(1994).
 CC -1- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL: S67520; G456899; -;
 DR PROSITE: P500249; PDGF: 1.
 KM MITOGEN: GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 7
 FT CHAIN 1 133
 FT DISULFID 36 78
 BY SIMILARITY.

FT DISULFID 67 112
 FT DISULFID 71 114
 FT DISULFID 61 61
 FT DISULFID 70 70
 FT CARBOHYD 85 85
 SQ SEQUENCE 133 AA: 14715 MW: E02EC395 CRC32:
 Query Match 78.5%; Score 95; DB 1; Length 133;
 Best Local Similarity 76.9%; Pred. No. 2.00e-07;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 59 PCVTLMRGCGC 71
 Qy 69 PSCVTYVRCGCGC 81
 RESULT 10
 ID VEGH_OREN7 STANDARD; PRT; 148 AA.
 AC P52585;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.
 GN A2R.
 OS ORF VIRUS (STRAIN N27).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHORDOPOXYVIRINAE;
 OC PARAPOXYVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 94076465.
 RA LITTLE D.J., FRASER K.M., FLEMING S.B., MERCER A.A., ROBINSON A.J.;
 RL J. VIROL. 68:84-92(1994).
 CC -1- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 DR EMBL: S67522; G456902; -;
 DR PROSITE: P500249; PDGF: FALSE-NEG.
 KM MITOGEN: GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 148
 FT CHAIN 1 148
 FT DISULFID 46 88
 FT DISULFID 77 130
 FT DISULFID 81 132
 FT DISULFID 71 71
 FT DISULFID 80 80
 FT CARBOHYD 95 95
 SQ SEQUENCE 148 AA: 16078 MW: E6B453C5 CRC32:
 Query Match 78.5%; Score 95; DB 1; Length 148;
 Best Local Similarity 76.9%; Pred. No. 2.00e-07;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 69 PCVTYVRCGCGC 81
 Qy 69 PSCVTYVRCGCGC 81
 RESULT 11
 ID VEGC_HUMAN STANDARD; PRT; 419 AA.
 AC P49767;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
 DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND).
 GN VEGF.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
 RA MEDLINE: 96178224.
 RX JOUKOV V., PAJUSOLA K., KAIPAINEN A., CHILOV D., LAHTINEN I.,

ID VEGF_PIG STANDARD: PRT: 190 AA.
AC P49151:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE: 95143284.
RA SHAWA H.S., TANG Z.H., GHO B.C.H., VERDOUM P.D.:
RL BIOCHIM. BIOPHYS. ACTA 1260:235-238(1995).
CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR EMBL: X81360; G587560; -
DR PROSITE: PS00249; PDGF: 1.
KW MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 26
FT CHAIN 27 190
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
SQ SEQUENCE 190 AA; 22368 MW; BA8CC907 CRC32;

Query Match 76.9%; Score 93; DB 1; Length 190;
Best Local Similarity 76.9%; Pred. No. 5.18e-07;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 74 PSCVPLMRCGCC 86
||||: |||||
QY 69 PSCVTQRCGCC 81

RESULT 15
ID VEGF_BOVIN STANDARD: PRT: 190 AA.
AC P15691:
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE: 90069608.
RA LEUNG D.W., CACHIANES G., KUANG W.-J., GOEDDEL D.V., FERRARA N.;
RL SCIENCE 246:1306-1309(1989).
RN [2]
RP SEQUENCE OF 27-190 FROM N.A.
RX MEDLINE: 90121225.
RA TISCHER E., GOSPODAROWICZ D., MITCHELL R., SILVA M., SCHILLING J., LAU K., CRISP T., FIDDES J.C., ABRAHAM J.A.,
RL BIOCHEM. BIOPHYS. RES. COMMUN. 165:1198-1206(1989).
RN [3]
RP SEQUENCE OF 27-31.
RX MEDLINE: 89286596.

RA FERRARA N., HENZEL W.J.:
RL BIOCHEM. BIOPHYS. RES. COMMUN. 161:851-858(1989).
CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR EMBL: M32976; G163007; -
DR EMBL: M31836; G163809; -
DR EMBL: M33750; G163811; -
DR PIR: A33255; A33255.
DR PIR: A33787; A33787.
DR PIR: B40080; B40080.
DR PROSITE: PS00249; PDGF: 1.
KW MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; ALTERNATIVE SPLICING; SIGNAL.
FT SIGNAL 1 26
FT CHAIN 27 190
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
FT VARSPLIC 139 183
FT VARSPLIC 184 184
SQ SEQUENCE 190 AA; 22310 MW; E22F67FD CRC32;

Query Match 76.9%; Score 93; DB 1; Length 190;
Best Local Similarity 76.9%; Pred. No. 5.18e-07;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 74 PSCVPLMRCGCC 86
||||: |||||
QY 69 PSCVTQRCGCC 81

Search completed: Thu Nov 26 00:01:39 1998
Job time : 8 secs.

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 M E S E R H
 (TM)

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Nov 26 00:00:38 1998; Maspar time 3.45 Seconds
 Tabular output not generated. 148.181 Million cell updates/sec

Title: >US-09-033-662-2
 Description: (69-82) from US09033662.pep
 Perfect Score: 121
 Sequence: 1 PSCVTVORCGCCP 14

Scoring table:
 PAM 150
 Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r56
 1:p1r1 2:p1r2 3:p1r3 4:p1r4 5:n1r13d

Statistics: Mean 23.485; Variance 43.203; scale 0.544

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description	Pred. No.
1	121	100.0	188	2	JC4680	3.68e-11
2	121	100.0	207	2	JC4679	3.68e-11
3	97	80.2	63	5	1PDG82	1.33e-06
4	97	80.2	66	5	1PDG82	1.33e-06
5	97	80.2	66	5	1PDG82	1.33e-06
6	97	80.2	161	2	18108	1.33e-06
7	97	80.2	185	2	S58383	1.33e-06
8	97	80.2	225	2	S25097	1.33e-06
9	97	80.2	226	1	TVMVSS	1.33e-06
10	97	80.2	230	2	A55030	1.33e-06
11	97	80.2	241	1	PFHUG2	1.33e-06
12	97	80.2	241	1	PFHUG2	1.33e-06
13	97	80.2	245	1	TVC7TS	1.33e-06
14	97	80.2	271	2	A25668	1.33e-06
15	95	78.5	133	2	B49530	3.11e-06
16	95	78.5	148	2	D49530	3.11e-06
17	94	77.7	419	2	S69207	4.77e-06
18	93	76.9	120	2	A33787	7.23e-06
19	93	76.9	146	2	S57956	7.23e-06
20	93	76.9	190	2	S52130	7.23e-06
21	93	76.9	190	2	B40080	7.23e-06
22	93	76.9	232	2	A41551	7.23e-06
23	88	72.7	166	2	JN0248	5.81e-05

24	88	72.7	196	2	A37359	platelet-derived grow	5.81e-05
25	88	72.7	196	2	B28964	platelet-derived grow	5.81e-05
26	88	72.7	196	2	A48651	platelet-derived grow	5.81e-05
27	88	72.7	197	2	S25095	platelet-derived grow	5.81e-05
28	88	72.7	198	2	JS0735	platelet-derived grow	5.81e-05
29	88	72.7	200	2	IS1531	platelet-derived grow	5.81e-05
30	88	72.7	211	1	PFHUG1	platelet-derived grow	5.81e-05
31	88	72.7	215	2	S08220	platelet-derived grow	5.81e-05
32	88	72.7	226	2	IS1550	platelet-derived grow	5.81e-05
33	87	71.9	128	2	IS1295	vascular endothelial	8.78e-05
34	87	71.9	190	2	B44881	vascular endothelial	8.78e-05
35	87	71.9	190	2	A35987	gloma-derived vascul	8.78e-05
36	87	71.9	214	2	A44881	vascular endothelial	8.78e-05
37	86	71.1	149	2	A41236	placental growth fact	1.32e-04
38	84	69.4	158	2	A56125	placental growth fact	3.00e-04
39	75	62.0	463	2	S75558	hypothetical protein	1.10e-02
40	63	52.1	143	2	B21761	high cysteine chorion	1.03e+00
41	63	52.1	392	2	A60777	keratin 2, type I, ha	1.03e+00
42	62	51.2	178	2	A23219	high-cysteine chorion	1.48e+00
43	61	50.4	438	2	C64148	hypothetical protein	2.13e+00
44	60	49.6	323	2	I48667	Mha3 (keratin acidic	3.04e+00
45	59	48.8	466	2	F69806	RNA methyltransferase	4.33e+00

ALIGNMENTS

RESULT ENTRY	1	ALIGNMENTS
TITLE	JC4680	#type complete
ALTERNATE_NAMES	vascular endothelial growth factor-related factor 167 - mouse	
ORGANISM	VR 167 protein	
DATE	10-May-1996	#formal_name Mus musculus #common_name house mouse
	10-Sep-1997	#sequence_revision 19-Jul-1996 #text_change

ACCESSIONS
 JC4680

REFERENCE
 JC4679

#authors

#journal

#title

#accession

#molecule_type mRNA

#residues

##cross-references GB:U3837; NID:g1314335; PID:g1314336

COMMENT

This factor is a mitogen, that is selective for endothelial cells,

and belongs to a family of growth factor. This transcript is

differentially spliced to produce two major isoforms, vascular

endothelial growth factors 167 and VEGF 186.

GENETICS

#gene

#map_position 19

#introns 137/2

FEATURE

1-21

22-188

SUMMARY

Query Match

Best Local Similarity 100.0%; Pred. No. 3.68e-11;

Matches 14; Conservative

Db

70 PSCVTVORCGCCP 83

Qy

69 PSCVTVORCGCCP 82

RESULT

2

ENTRY

ALTERNATE_NAMES

ORGANISM

DATE

10-Sep-1997

10-Sep-1997

10-Sep-1997

ACCESSIONS JC4679
REFERENCE JC4679
#authors Townson, S.; Jagerant, J.; Grimmond, S.; Sillis, G.;
Nordenskjold, M.; Weber, G.; Hayward, N.
#journal Biochem. Biophys. Res. Commun. (1996) 220:922-928
#title Characterization of the murine VEGF-related factor gene.
#accession JC4679
#molecule_type mRNA
#residues 1-207
#label TOW
#cross-references GB:U43836; NID:q1703480; PID:q1314334
COMMENT This factor is a mitogen, that is selective for endothelial cells,
and belongs to a family of growth factors. This transcript is
differentially spliced to produce two major isoforms, vascular
endothelial growth factors 167 and 186.

GENETICS
#gene vrf
#map_position 19
KEYWORDS growth factor
FEATURE
1-21
22-207

SUMMARY #domain signal sequence #status predicted #label SIG
#product vascular endothelial growth factor related
factor #status predicted #label MAT
#length 207 #molecular_weight 21914 #checksum 1525

Query Match 100.0%; Score 121; DB 5; Length 207;
Best Local Similarity 100.0%; Pred. No. 3.68e-11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 PSCVTQRCGCCP 83
QY 69 PSCVTQRCGCCP 82

RESULT 3
ENTRY 1PDGB2 #type fragment
TITLE Platelet-derived growth factor db, chain B, fragment 2 -
ORGANISM human
#formal_name Homo sapiens #common_name man
#note recombinant form expressed in (saccharomyces cerevisiae)
REFERENCE A51904
#authors Oefner, C.; Darcy, A.D.; Winkler, F.K.; Eggmann, B.; Hosang,
M.
#submission submitted to the Brookhaven Protein Data Bank, July 1992
#cross-references PDB:1PDG
REFERENCE TN011667
#authors Oefner, C.; D'Arcy, A.; Winkler, F.K.; Eggmann, B.; Hosang,
M.
#journal EMBO J. (1992) 11:3921
#title Crystal structure of human platelet-derived growth factor bb.
COMMENT Resolution: 3.0 angstroms
KEYWORDS Determination: X-ray diffraction
FEATURE Growth factor
5-13 #region beta sheet\
21-40, 44-63 #region beta sheet\
18-21 #region turn\
41-44 #region turn\
15 #disulfide_bonds interchain (to 1PDGA2:6)\
6 #disulfide_bonds interchain (to 1PDGA2:15)\
23 #disulfide_bonds interchain (to 1PDGB1:10)\
12-60 #disulfide_bonds\
16-62 #disulfide_bonds
SUMMARY #length 63 #checksum 9137

Query Match 80.2%; Score 97; DB 5; Length 63;
Best Local Similarity 76.9%; Pred. No. 1.33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 4 PSCVEVORCGGCC 16
QY 69 PSCVTQRCGCC 81

RESULT 4
ENTRY 1PDGC2 #type fragment
TITLE Platelet-derived growth factor bb, chain C, fragment 2 -
ORGANISM human
#formal_name Homo sapiens #common_name man
#note recombinant form expressed in (saccharomyces cerevisiae)
REFERENCE A51904
#authors Oefner, C.; Darcy, A.D.; Winkler, F.K.; Eggmann, B.; Hosang,
M.
#submission submitted to the Brookhaven Protein Data Bank, July 1992
#cross-references PDB:1PDG
REFERENCE TN011671
#authors Oefner, C.; D'Arcy, A.; Winkler, F.K.; Eggmann, B.; Hosang,
M.
#journal EMBO J. (1992) 11:3921
#title Crystal structure of human platelet-derived growth factor bb.
COMMENT Resolution: 3.0 angstroms
KEYWORDS Determination: X-ray diffraction
FEATURE Growth factor
6-14 #region beta sheet\
22-41, 45-65 #region beta sheet\
19-22 #region turn\
42-45 #region turn\
24 #disulfide_bonds interchain (to 1PDG1:10)\
13-61 #disulfide_bonds\
17-63 #disulfide_bonds
SUMMARY #length 66 #checksum 1405

Query Match 80.2%; Score 97; DB 5; Length 66;
Best Local Similarity 76.9%; Pred. No. 1.33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 5 PSCVEVORCGGCC 17
QY 69 PSCVTQRCGCC 81

RESULT 5
ENTRY 1PDGB2 #type fragment
TITLE Platelet-derived growth factor db, chain A, fragment 2 -
ORGANISM human
#formal_name Homo sapiens #common_name man
#note recombinant form expressed in (saccharomyces cerevisiae)
REFERENCE A51904
#authors Oefner, C.; Darcy, A.D.; Winkler, F.K.; Eggmann, B.; Hosang,
M.
#submission submitted to the Brookhaven Protein Data Bank, July 1992
#cross-references PDB:1PDG
REFERENCE TN011667
#authors Oefner, C.; D'Arcy, A.; Winkler, F.K.; Eggmann, B.; Hosang,
M.
#journal EMBO J. (1992) 11:3921
#title Crystal structure of human platelet-derived growth factor bb.
COMMENT Resolution: 3.0 angstroms
KEYWORDS Determination: X-ray diffraction
FEATURE Growth factor
6-14 #region beta sheet\
22-41, 45-65 #region beta sheet\
19-22 #region turn\
42-45 #region turn\
24 #disulfide_bonds interchain (to 1PDGA1:8)\
13-61 #disulfide_bonds interchain (to 1PDGB2:16)\
16 #disulfide_bonds interchain (to 1PDGB2:7)\
17-63 #disulfide_bonds
SUMMARY #length 68 #checksum 2770

Query Match 80.2%; Score 97; DB 5; Length 68;
Best Local Similarity 76.9%; Pred. No. 1.33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 5 PCCEVORCGGCC 17
1:1111111111
OY 69 PSCVTWORCGGCC 81

RESULT 6
ENTRY 138108 #type complete
TITLE platelet-derived growth factor-BB - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
09-May-1997

ACCESSIONS
REFERENCE 138108
#authors Cook, A.L.; Kirwin, P.M.; Craig, S.; Bawden, L.J.; Green,
D.R.; Price, M.J.; Richardson, S.J.; Fallon, A.; Drummond,
A.H.; Edwards, R.M.; Clements, J.M.
#journal Biochem. J. (1992) 281:57-65
#title Purification and analysis of proteinase-resistant mutants of
recombinant platelet-derived growth factor-BB exhibiting
improved biological activity.
#cross-references NUID:92117992
#accession 138108
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-161 #label RES
#cross-references EMBL:X63966; NID:g311378; PID:g35377
CLASSIFICATION #superfamily platelet-derived growth factor
SUMMARY #length 161 #molecular_weight 18237 #checksum 8276

Query Match 80.2% Score 97; DB 2; Length 161;
Best Local Similarity 76.9%; Pred. No. 1.33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 42 PCCEVORCGGCC 54
1:1111111111
OY 69 PSCVTWORCGGCC 81

RESULT 7
ENTRY 558383 #type complete
TITLE hypothetical protein 2 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
20-Feb-1998

ACCESSIONS
REFERENCE 558383
#authors Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.;
Bloemers, H.P.J.
#journal Nucleic Acids Res. (1995) 23:2815-2822
#title A novel human c-sis mRNA species is transcribed from a
promoter in c-sis intron 1 and contains the code for an
alternative PDGF-B-like protein.
#accession 558383
#status preliminary
#molecule_type mRNA
#residues 1-185 #label DIR
#cross-references EMBL:X83705
SUMMARY #length 185 #molecular_weight 20774 #checksum 2728

Query Match 80.2% Score 97; DB 2; Length 185;
Best Local Similarity 76.9%; Pred. No. 1.33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 107 PCCEVORCGGCC 119
1:1111111111
OY 69 PSCVTWORCGGCC 81

RESULT 8
ENTRY S25097 #type fragment
TITLE platelet-derived growth factor chain B precursor - rat
(fragment)
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
08-Sep-1997

ACCESSIONS
REFERENCE S25097; S33765; 152866
#authors Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
#submission Submitted to the EMBL Data Library, July 1992
#description Cross-species conservation in sequence and function of PDGF
ligands and receptors.
#accession S25097
#molecule_type mRNA
#residues 1-225 #label HER1
#cross-references EMBL:Z14117; NID:g56867; PID:g56868
REFERENCE S33764
#authors Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
#journal Biochim. Biophys. Acta (1993) 1173:294-302
#title Conservation in sequence and affinity of human and rodent
PDGF ligands and receptors.
#accession S33765
#molecule_type mRNA
#residues 89-172 #label HER2
#cross-references EMBL:Z14117
REFERENCE 152866
#authors Lindner, V.; Giachelli, C.M.; Schwartz, S.M.; Reidy, M.A.
#journal Circ. Res. (1995) 76:951-957
#title A subpopulation of smooth muscle cells in injured rat
arteries expresses platelet-derived growth factor-B chain
mRNA.
#cross-references NUID:95277908
#accession 152866
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 74-182 #label RES
#cross-references GB:L40991; NID:g727177; PID:g727178

GENETICS
#gene PDGF-B
CLASSIFICATION #superfamily platelet-derived growth factor
KEYWORDS growth factor; mitogen; platelet
SUMMARY #length 225 #checksum 2584

Query Match 80.2% Score 97; DB 2; Length 225;
Best Local Similarity 76.9%; Pred. No. 1.33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 114 PCCEVORCGGCC 126
1:1111111111
OY 69 PSCVTWORCGGCC 81

RESULT 9
ENTRY T24555 #type complete
TITLE PGF-related transforming protein (sis) - simian sarcoma
virus
ALTERNATE_NAMES p28-sis
ORGANISM #formal_name simian sarcoma virus
DATE 23-Jul-1983 #sequence_revision 20-Sep-1984 #text_change
31-Oct-1997

ACCESSIONS
REFERENCE A01381
#authors Devare, S.G.; Reddy, E.P.; Iaw, J.D.; Robbins, K.C.;
Aaronson, S.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1983) 80:731-735
#title Nucleotide sequence of the simian sarcoma virus genome:
demonstration that its acquired cellular sequences encode
the transforming gene product p28(sis).
#cross-references NUID:83144004
#accession A01381
#molecule_type genomic RNA
#residues 1-226 #label DEV

GENETICS
#gene sis
CLASSIFICATION #superfamily platelet-derived growth factor
KEYWORDS growth factor; transforming protein
FEATURE

```

6-226      #domain platelet-derived growth factor chain B
SUMMARY    #length 226 #molecular-weight 25411 #checksum 2886

Query Match
Best Local Similarity 80.2%; Score 97; DB 1; Length 226;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 107 PCVEVORCGGCC 119
QY 69 PSCVTVORCGGCC 81

RESULT 10
ENTRY    #type fragment
TITLE    platelet-derived growth factor chain B precursor - human
          (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE      18-Nov-1994 #sequence-revision 18-Nov-1994 #text-change
          03-May-1996
ACCESSION A55030
REFERENCE A55030
AUTHORS   Johnson, A.; Heldin, C.H.; Wasteson, A.; Westermark, B.;
          Denel, T.F.; Huang, J.S.; Seeburg, P.H.; Gray, A.; Ullrich,
          A.; Scerace, G.; Stroobant, P.; Waterfield, M.D.
          EMBO J. (1984) 3:921-928
          The c-sis gene encodes a precursor of the B chain of
          platelet-derived growth factor.
          #accession A55030
          #status preliminary
          #molecule-type DNA
          #residues 1-230 #label JOH
          #cross-references GB:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562
CLASSIFICATION #superfamily platelet-derived growth factor
SUMMARY        #length 230 #checksum 3580

Query Match
Best Local Similarity 80.2%; Score 97; DB 2; Length 230;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 111 PCVEVORCGGCC 123
QY 69 PSCVTVORCGGCC 81

RESULT 11
ENTRY    #type complete
TITLE    platelet-derived growth factor chain B precursor - human
          PDGF B-chain; PDGF-B; PDGF-IT; PDGF-related transforming
          protein (sis)
ALTERNATE_NAMES
ORGANISM #formal name Homo sapiens #common name man
DATE      18-Apr-1984 #sequence-revision 20-Sep-1984 #text-change
          20-Mar-1998
ACCESSION A94776; A21024; A23532; A93366; A25141; A94271; A93308;
          A43499; S56115; I57635; I37266; A01380; A94622
REFERENCE A94276
AUTHORS   Josephs, S.F.; Ratner, L.; Clarke, M.F.; Westin, E.H.; Reitz,
          M.S.; Wong-Staal, F.
          Science (1984) 225:636-639
          Transforming potential of human c-sis nucleotide sequences
          encoding platelet-derived growth factor.
          #cross-references MUID:84250225
          #accession A94276
          #molecule-type DNA
          #residues 1-241 #label JOS
REFERENCE #cross-references GB:K01401; NID:9338206; PID:9338209
A21024
AUTHORS   Chin, I.M.; Reddy, E.P.; Glivol, D.; Robbins, K.C.; Tronick,
          S.R.; Aaronson, S.A.
          Cell (1984) 37:123-129
          Nucleotide sequence analysis identifies the human c-sis
          proto-oncogene as a structural gene for platelet-derived
          growth factor.

#cross-references MUID:84205633
#accession A21024
#molecule-type DNA
#residues 17-20,'RQ',22-241 #label CH2
REFERENCE A23532
AUTHORS   Rao, C.D.; Igarashi, H.; Chiu, I.M.; Robbins, K.C.; Aaronson,
          S.A.
          Proc. Natl. Acad. Sci. U.S.A. (1986) 83:2392-2396
          Structure and sequence of the human c-sis/platelet-derived
          growth factor 2 (sis/PDGF2) transcriptional unit.
          #cross-references MUID:86205961
          #accession A23532
          #molecule-type mRNA
          #residues 1-241 #label RAO
REFERENCE #cross-references GB:M12783; GB:M16288; NID:9338210; PID:9338211
A93366
AUTHORS   Collins, T.; Ginsburg, D.; Boss, J.M.; Orkin, S.H.; Pober,
          J.S.
          Nature (1985) 316:748-750
          Cultured human endothelial cells express platelet-derived
          growth factor B chain: cDNA cloning and structural
          analysis.
          #cross-references MUID:85296313
          #accession A93366
          #molecule-type mRNA
          #residues 1-241 #label COL
REFERENCE #cross-references GB:X02811; NID:935371; PID:935372
A25141
AUTHORS   Welch, H.A.; Sebald, W.; Schaller, H.U.; Hoppe, J.
          FEBS Lett. (1986) 198:344-348
          The human osteosarcoma cell line U-2 OS expresses a 3.8
          kilobase mRNA which codes for the sequence of the PDGF-B
          chain.
          #cross-references MUID:86164981
          #accession A25141
          #molecule-type mRNA
          #residues 26-241 #label WEI
REFERENCE #cross-references GB:X03702; NID:935374; PID:935375
A94271
AUTHORS   Antonlades, H.N.; Hunkapiller, M.W.
          Science (1983) 220:963-965
          Human platelet-derived growth factor (PDGF): amino-terminal
          amino acid sequence.
          #cross-references MUID:83197379
          #accession A94271
          #molecule-type protein
          #residues 82-100,'E',102-104,'C',106,'C',108-110 #label ANT
REFERENCE A93308
AUTHORS   Waterfield, M.D.; Scerace, G.T.; Whittle, N.; Stroobant, P.;
          Johnson, A.; Wasteson, A.; Westermark, B.; Heldin, C.H.;
          Huang, J.S.; Denel, T.F.
          Nature (1983) 304:35-39
          Platelet-derived growth factor is structurally related to the
          putative transforming protein p28(sis) of simian sarcoma
          virus.
          #cross-references MUID:83244981
          #accession A93308
          #molecule-type protein
          #residues 82-112 #label WAT
REFERENCE A43499
AUTHORS   Josephs, S.F.; Guo, C.; Ratner, L.; Wong-Staal, F.
          Science (1984) 223:487-491
          Human proto-oncogene nucleotide sequences corresponding to
          the transforming region of simian sarcoma virus.
          #accession A43499
          #status not compared with conceptual translation
          #molecule-type DNA
          #residues 'Q',22-241 #label JO2
REFERENCE S56115
AUTHORS   Lu, K.V.; Rode, M.F.; Thomason, A.R.; Kenney, W.C.; Lu, H.S.
          Biochem. J. (1995) 309:411-417
          Mistranslation of a TGA termination codon as tryptophan in
          recombinant platelet-derived growth factor expressed in

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#accession      EScherichia coli.
#status         S56115
#molecule_type preliminary
#residues       82-93 ##label LUK
REFERENCE
#authors         Rao, C.D.; Pech, M.; Robbins, K.C.; Aaronson, S.A.
#journal         Mol. Cell. Biol. (1988) 8:284-292
#title           The 5' untranslated sequence of the c-sis/platelet-derived
                  growth factor 2 transcript is a potent translational
                  inhibitor.
#cross-references MUID:88094398
#accession      157635
#status         translated from GB/EMBL/DBDJB
#molecule_type DNA
#residues       1-20 ##label RES
#cross-references GB:M19719; NID:g189727; PID:g553608
REFERENCE
#authors         Ratner, L.; Josephs, S.F.; Jarrett, R.; Reitz, M.S.
#journal         Nucleic Acids Res. (1985) 13:5007-5018
#title           Nucleotide sequence of transforming human c-sis cDNA clones
                  with homology to platelet-derived growth factor.
#cross-references MUID:85269623
#accession      137266
#status         translated from GB/EMBL/DBDJB
#molecule_type mRNA
#residues       1-241 ##label RE2
#cross-references EMBL:X02744; NID:g30246; PID:g30247
COMMENT
#text            The receptor for this growth factor is a tyrosine kinase.
                  Human platelet-derived growth factor, a potent mitogen for cells of
                  mesenchymal origin, is a disulfide-linked dimer of two chains,
                  which may be both of type A, both of type B, or an A-B
                  heterodimer. Reduction of its disulfide bonds irreversibly
                  destroys biological activity. Different receptors bind
                  preferentially to A-A and B-B homodimers. This growth factor
                  induces a variety of cellular responses.
                  B and A chains are encoded by genes located on different
                  chromosomes. The two genes are expressed independently in human
                  tumor cell lines.
COMMENT
#text            GDB:PDGFB
#gene           #cross-references GDB:120709; OMIM:190040
#map_position   22q12.3-22q13.1
#intons         57/3; 94/1; 192/3; 241/1
CLASSIFICATION #superfamily platelet-derived growth factor
KEYWORDS        growth factor; mitogen
FEATURE
1-20            #domain signal sequence #status predicted #label SIG
21-81          #domain amino-terminal propeptide #status predicted
82-190         #product platelet-derived growth factor chain B #status
                  #label PRO\
159-163        #region receptor binding #status predicted\
191-241        #domain carboxyl-terminal propeptide #status predicted
                  #label CTR\
97-141,130-178,
134-180        #disulfide_bonds #status experimental\
124            #disulfide_bonds interchain (to 133 in homodimeric form)
                  #status experimental\
124            #disulfide_bonds interchain (to chain A-132 in
                  heterodimeric form) #status predicted\
133            #disulfide_bonds interchain (to 124 in homodimeric form)
                  #status experimental\
133            #disulfide_bonds interchain (to chain A-124 in
                  heterodimeric form) #status predicted
SUMMARY
#length 241 #molecular_weight 27283 #checksum 3348
Query Match      80.2%; Score 97; DB 1; Length 241;
Best Local Similarity 76.9%; Pred. No. 1,33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
1:11 11111:111

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OY      69   PSCVTVORCGGCC 81

RESULT    12          PFMSGB      #type complete
ENTRY     .           platelet-derived growth factor chain B precursor (sis) - mouse
TITLE                                          
ALTERNATE_NAMES PDGF-related transforming protein
ORGANISM       #format_name Mus musculus #common_name house mouse
DATE           31-Dec-1992 #sequence_revision 31-Mar-1993 #text_change 24-Oct-1997
ACCESSIONS    A39073
REFERENCE     Bonthonron, D.T.; Sultan, P.; Collins, T.
#authors      Genomics (1991) 10:287-292.
#journal      Structure of the murine c-sis proto-oncogene (Sis, PDGFB) encoding the B chain of platelet-derived growth factor.
#title        #cross-references MIMD:91257844
#cross-refere A39073
#accession    ##molecule_type DNA
#residues     ##residues 1-241 ##label BON
#cross-refere #cross-references GB:M64849; GB:W55394; NID:g192818; PID:g192820

GENETICS      sis
CLASSIFICATION #superfamily platelet-derived growth factor
KEYWORDS      glycoprotein; growth factor; platelet; proto-oncogene; transforming protein

FEATURE
1-20          #domain signal sequence #status predicted #label SIG\
21-81         #domain propeptide #status predicted #label PRO\
82-190        #product platelet-derived growth factor chain B #status predicted #label MAT\

159-163       #region receptor binding #status predicted\
63            #binding_site carbohydrate (asn) (covalent) #status predicted

SUMMARY       #length 241 #molecular_weight 27381 #checksum 4345

Query Match 80.2%; Score 97; DB 1; Length 241;
Best Local Similarity 76.9%; Pred. NO. 1.33e-06;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      122   PCVEVORCGGCC 134
OY      69   PSCVTVORCGGCC 81
1:|||||1|||1|

RESULT    13          TVCRSS      #type complete
ENTRY     .           platelet-derived growth factor chain B precursor - cat
TITLE                                          
ALTERNATE_NAMES PDGF-related transforming protein
ORGANISM       #format_name Felis silvestris catus #common_name domestic cat
DATE           30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Mar-1996
ACCESSIONS    A26402
REFERENCE     Van den Ouweland, A.M.W.; Van Groningen, J.J.M.; Schalken, J.A.J.; Van Neck, H.W.; Bloemers, H.P.J.; Van de Ven, W.J.M.
#authors      Nucleic Acids Res. (1987) 15:959-970
#journal      Genetic organization of the c-sis transcription unit.
#title        #cross-references MIMD:87146463
#accession    A26402
#molecule_type mRNA
#residues     ##residues 1-245 ##label VAN

GENETICS      sis
CLASSIFICATION #superfamily platelet-derived growth factor
KEYWORDS      glycoprotein; growth factor; platelet; proto-oncogene; transforming protein

FEATURE
1-20          #domain signal sequence #status predicted #label SIG\
21-81         #domain propeptide #status predicted #label PRO\
82-194        #product platelet-derived growth factor chain B #status predicted #label MAT\

```

163-167 #region receptor binding #status predicted\
63 #binding_site carbohydrate (Asn) (covalent) #status
predicted

SUMMARY #length 245 #molecular-weight 27787 #checksum 2148

Query Match 80.2%; Score 97; DB 1; Length 245;

Best Local Similarity 76.9%; Pred. No. 1.33e-06;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 126 PPCVEVORCGGCC 138

OY 69 PSCVTYORCGGCC 81

RESULT 14

ENTRY A25669 #type complete
TITLE PDGF-related transforming protein (v-sis) - simian sarcoma

ORGANISM #formal_name simian sarcoma virus
DATE 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change
12-Apr-1995

ACCESSIONS A25669
REFERENCE A25669
#authors Hamink, M.; Sauer, M.K.; Donoghue, D.J.
#journal Mol. Cell. Biol. (1986) 6:1304-1314
#cross-references MUID:87064399
#accession A25669

#status preliminary
#molecule_type protein
#residues 1-271 #label HAN

#note deletions in the C-terminal Coding Region of the v-sis
Gene: Dimerization is Required for Transformation

CLASSIFICATION #superfamily platelet-derived growth factor
SUMMARY #length 271 #molecular-weight 30108 #checksum 5973

Query Match 80.2%; Score 97; DB 2; Length 271;

Best Local Similarity 76.9%; Pred. No. 1.33e-06;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 152 PPCVEVORCGGCC 164

OY 69 PSCVTYORCGGCC 81

RESULT 15

ENTRY B49530 #type complete
TITLE vascular endothelial growth factor homolog A2R, 14.7K - Orf

ORGANISM #formal_name Orf virus
DATE 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1998

ACCESSIONS B49530
REFERENCE A49530
#authors Lytle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.;
Robinson, A.J.

#journal J. Virol. (1994) 68:84-92

#title Homologs of vascular endothelial growth factor are encoded by
the poxvirus orf virus.

#cross-references MUID:94076465

#contents NZ2

#accession B49530

#status preliminary

#molecule_type DNA

#residues 1-133 #label LYT

#cross-references GB:S67520; NID:q456897; PID:q456899

#note sequence inconsistent with nucleotide translation

#note sequence extracted from NCBI backbone (NCBIN:141420,
NCBIP:141425)

SUMMARY #length 133 #molecular-weight 14729 #checksum 8681

Query Match

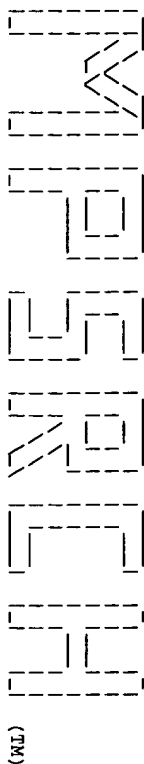
Best Local Similarity 78.5%; Score 95; DB 2; Length 133;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 59 PSCVTIMRCGGCC 71

OY 69 PSCVTYORCGGCC 81

Search completed: Thu Nov 26 00:01:13 1998
Job time : 35 secs.



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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Nov 25 23:59:51 1998; Maspar time 2.92 Seconds

Tabular output not generated. 77,454 Million cell updates/sec

Title: >US-09-033-662-2
Description: (469-82) from US09033662.pep
Perfect Score: 121
Sequence: 1 PSCVTVQRCGGCCP 14

Scoring table:
PAM 150
Gap 11

Searched: 131922 seqs, 16180650 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 17.247; Variance 67.281; scale 0.256

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	121	100.0	101 19	W00728	Vascular endothelial	6.08e-05
2	121	100.0	102 21	W04824	Vascular endothelial	6.08e-05
3	121	100.0	133 21	W04828	Vascular endothelial	6.08e-05
4	121	100.0	143 19	W00727	Vascular endothelial	6.08e-05
5	121	100.0	188 21	W04829	Fibrosarcoma vascular	6.08e-05
6	121	100.0	188 19	W00864	Murine VRF167.	6.08e-05
7	121	100.0	188 19	W00726	Vascular endothelial	6.08e-05
8	121	100.0	188 21	W04826	Vascular endothelial	6.08e-05
9	121	100.0	195 21	W04827	Heart vascular endoth	6.08e-05
10	121	100.0	207 19	W00863	Murine VRF186.	6.08e-05
11	121	100.0	207 19	W00725	Vascular endothelial	6.08e-05
12	121	100.0	207 21	W04831	Vascular endothelial	6.08e-05
13	121	100.0	207 21	W04830	Vascular endothelial	6.08e-05
14	121	100.0	221 23	W06111	Human vascular endoth	5.63e-05
15	101	83.5	620 22	W14994	Human C-Fos induced g	1.38e-02
16	97	80.2	109 4	R20967	PDGF-B.	1.38e-02
17	97	80.2	109 4	R20967	Sequence of B-chain o	1.38e-02
18	97	80.2	109 3	P81030	Sequence of mature B-	1.38e-02

19	97	80.2	109 5	R25443	PDGF analogue #3.	1.38e-02
20	97	80.2	109 16	R87515	PDGF mosaic peptide B	1.38e-02
21	97	80.2	110 12	R86519	Mature human PDGF-B.	1.38e-02
22	97	80.2	110 16	R87517	PDGF mosaic peptide B	1.38e-02
23	97	80.2	114 6	R04020	PDGF-BB monomer unit.	1.38e-02
24	97	80.2	114 1	P80163	Biosynthetic multilin	1.38e-02
25	97	80.2	120 3	R12879	PDGF-B19 from PCFM1	1.38e-02
26	97	80.2	120 8	R41523	PDGF-B19 from PCFM1	1.38e-02
27	97	80.2	120 12	R67261	PDGF-B19	1.38e-02
28	97	80.2	120 12	R60614	Human PDGF-B 119 subu	1.38e-02
29	97	80.2	130 10	R50012	Truncated Platelet de	1.38e-02
30	97	80.2	130 12	R50015	Human PDGF-B 109 subu	1.38e-02
31	97	80.2	216 12	R68617	Human PDGF-B precursor	1.38e-02
32	97	80.2	220 12	R63470	Recombinant platelet	1.38e-02
33	97	80.2	226 2	R25673	Recombinant platelet	1.38e-02
34	97	80.2	226 3	P60215	Sequence encoded by t	1.38e-02
35	97	80.2	241 8	R40964	PDGF-Bc-sis.	1.38e-02
36	97	80.2	241 10	R50002	Platelet-derived Grow	1.38e-02
37	97	80.2	241 12	R63472	Recombinant platelet	1.38e-02
38	97	80.2	241 10	R50009	Platelet-derived Grow	1.38e-02
39	97	80.2	241 12	R63469	Recombinant platelet	1.38e-02
40	97	80.2	241 1	P80596	Recombinant platelet	1.38e-02
41	97	80.2	256 12	R63473	CGH/PGDF B fusion pro	1.38e-02
42	97	80.2	256 8	R40968	CGH/PGDF Bv-sis fusio	1.38e-02
43	97	80.2	271 12	R63468	Recombinant platelet	1.38e-02
44	97	80.2	271 1	P80595	Recombinant platelet	1.38e-02
45	97	80.2	282 12	R60616	Human PDGF-B 119 link	1.38e-02

ALIGNMENTS

RESULT 1
W00728 standard; Protein; 101 AA.

ID W00728; (first entry)
AC 30-NOV-1996
DE Vascular endothelial growth factor-like protein SOM175-e4.
KW Vascular endothelial growth factor; VEGF; SOM175-e4; neuron;
OS astroglial proliferation.
FH Homo sapiens.
FT Key peptide
FT Location/Qualifiers
FT 1..21
FT /label= Sig_peptide
PN W09627007-A1.
PD 06-SEP-1996.
PF 22-FEB-1996; AU0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI: 96-412774/41.
DR N-PSDB: T33613.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival.
PS Claim 14; Page 48; 113pp; English.
CC Splice variants (W00726-28) of the human vascular endothelial growth
CC factor-like polypeptide SOM175 (see also W00725) are products of
CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
CC 6-7, and exon 4 of the SOM175 gene (see also T33610). They show at
CC least 1 of the properties of SOM175 including the ability to induce
CC proliferation of vascular endothelial cells, to interact with
CC fit-1/fil-1 receptors, and to induce cell migration, cell survival
CC and/or an increase in intracellular levels of alkaline phosphatase.
CC Recombinant SOM175 proteins can be used to induce astroglial
CC proliferation and to promote neural survival and/or proliferation.
SQ Sequence 101 AA;

Query Match 100.0%; Score 121; DB 19; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.08e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC factor-like polypeptide SOM175 (see also W00725) are products of
 CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
 CC 6-7, and exon 4 of the SOM175 gene (see also T33610). They show at
 CC least 1 of the properties of SOM175 including the ability to induce
 CC proliferation of vascular endothelial cells, to interact with
 CC flt-1/flk-1 receptors, and to induce cell migration, cell survival
 CC and/or an increase in intracellular levels of alkaline phosphatase.
 CC Recombinant SOM175 proteins can be used to induce astroglial
 CC proliferation and to promote neural survival and/or proliferation.
 SO Sequence 143 AA;

Query Match 100.0%; Score 121; DB 19; Length 143;
 Best Local Similarity 100.0%; Pred. No. 6.06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvgrcgccp 83
 |||||||
 QY 69 pscvtvgrcgccp 82

RESULT 5
 ID W04829 standard; Protein; 188 AA.
 DT 28-APR-1997 (first entry)
 DE Fibrosarcoma vascular endothelial growth factor-B167.
 KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse.
 OS Homo sapiens.
 PN W09626736-A1.
 PD 06-SEP-1996.
 PF 01-MAR-1996; U02957.
 PR 01-MAR-1995; US-397651.
 PR 06-JUN-1995; US-469427.
 PR 06-DEC-1995; US-569063.
 PA (LUDM-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 PI Allitalo K, Eriksson U, Olofsson B, Pajusola K;
 DR WPI: 96-412582/41.
 DR N-PSDB: T37913.
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis
 PS Claim 18: Page 59; 107pp; English.
 CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
 CC proteins of the invention, which promote endothelial or mesodermal cell
 CC proliferation. VEGF is also a glycosylated cationic dimer, and is
 CC sometimes referred to as vascular permeability factor (VPF). VEGF has
 CC diverse effects, depending on the specific biological context in which it
 CC is found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting endothelial
 CC cell growth during normal embryonic development, wound healing, and
 CC tissue regeneration/reorganisation. The VEGF proteins of the invention
 CC share the angiogenic and other properties of VEGF, but are distributed
 CC and expressed in tissues differently to VEGF. The proteins can therefore
 CC be used to accelerate angiogenesis in wound healing. Antibodies against
 CC the proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences direct against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.
 SO Sequence 188 AA;

Query Match 100.0%; Score 121; DB 21; Length 188;
 Best Local Similarity 100.0%; Pred. No. 6.06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvgrcgccp 83

QY 69 pscvtvgrcgccp 82
 |||||||

RESULT 6
 ID W00864 standard; Protein; 188 AA.
 AC W00864;
 DT 30-NOV-1996 (first entry)
 DE Murine VRF167.
 KW VRF: vascular endothelial growth factor; VEGF; SOM175; neuron;
 KW astroglial proliferation.
 OS Mus musculus.
 FH Key
 FT peptide
 FT peptide 1..21 /label= sig_peptide
 PN W09627007-A1.
 PD 06-SEP-1996.
 PF 22-FEB-1996; AU0094.
 PR 02-MAR-1995; AU-001457.
 PR 20-NOV-1995; AU-006647.
 PR 22-DEC-1995; AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
 PI Weber G;
 DR WPI: 96-412774/41.
 DR N-PSDB: T13810.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival
 PS Example 5; Fig 9; 113pp; English.
 CC VRF167 (W00863) is the murine homologue of an alternatively spliced
 CC variant (W00726) of human vascular endothelial growth factor-like
 CC polypeptide SOM175 (W00725), a protein capable of inducing astroglial
 CC proliferation and of promoting neural survival and/or proliferation.
 CC Its amino acid sequence was deduced from a cDNA clone (T13810)
 CC isolated from a new-born mouse brain cDNA library. VRF167 shows
 CC 85% identity and 92% similarity to its human counterpart. It lacks
 CC 101 amino acids found in VRF186 (W00865), the murine homologue
 CC of SOM175, owing to a deletion of exon 6 during splicing.
 SO Sequence 188 AA;

Query Match 100.0%; Score 121; DB 19; Length 188;
 Best Local Similarity 100.0%; Pred. No. 6.06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvgrcgccp 83
 |||||||

RESULT 7
 ID W00726 standard; Protein; 188 AA.
 AC W00726;
 DT 30-NOV-1996 (first entry)
 DE Vascular endothelial growth factor-like protein SOM175-e6.
 KW Vascular endothelial growth factor; VEGF; SOM175-e6; neuron;
 KW astroglial proliferation.
 OS Homo sapiens.
 FH Key
 FT peptide
 FT peptide 1..21 /label= sig_peptide
 PN W09627007-A1.
 PD 06-SEP-1996.
 PF 22-FEB-1996; AU0094.
 PR 02-MAR-1995; AU-001457.
 PR 20-NOV-1995; AU-006647.
 PR 22-DEC-1995; AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
 PI Weber G;
 DR WPI: 96-412774/41.
 DR N-PSDB: T33611.
 PT New growth factor related to vascular endothelial growth factor -

PT useful for inducing astroglial proliferation and promoting neuronal survival
PS Claim 12: Page 42-43; 113pp; English.
CC Splice variants (W00726-28) of the human vascular endothelial growth factor-like polypeptide SOM175 (see also W00725) are products of
CC CDNA clones (see also T33611-13) respectively lacking exon 6, exons 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at least 1 of the properties of SOM175 including the ability to induce proliferation of vascular endothelial cells, to interact with flt-1/flk-1 receptors, and to induce cell migration, cell survival and/or an increase in intracellular levels of alkaline phosphatase.
CC Recombinant SOM175 proteins can be used to induce astroglial proliferation and to promote neural survival and/or proliferation.
SQ Sequence 188 AA;

Query Match 100.0%; Score 121; DB 19; Length 188;
Best Local Similarity 100.0%; Pred. No. 6,06e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvqrcgccc 83
|||
QY 69 pscvtvqrcgccc 82

RESULT 8
ID W04826 standard; Protein: 188 AA.
AC W04826;
DT 28-APR-1997 (first entry)
DE Heart vascular endothelial growth factor-B167.
KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF; VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration; vascular permeability factor; cell mitogen; angiogenesis; cell growth; embryonic development; wound healing; tissue reorganisation; antibody; cancer; metastatic risk; tumour cell; mouse.
OS Mus musculus.
PN W09626736-A1.
PD 06-SEP-1996.
PF 01-MAR-1996; U02957.
PR 01-MAR-1995; US-397651.
PR 06-JUN-1995; US-469427.
PR 06-DEC-1995; US-569063.
PA (LUDM-) LUDWIG INST CANCER RES.
PI (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
DR WPI: 96-412582/41.
DR N-PSDB: T37910.
PT Vascular endothelial growth factor VEGF-B proteins - useful to accelerate angiogenesis in wound healing, also related nucleic acid and antibodies for cancer diagnosis.
PS Claim 18: Page 55-56; 107pp; English.
CC W04824-W04831 represent the vascular endothelial growth factor (VEGF) proteins of the invention, which promote endothelial or mesodermal cell proliferation. VEGF is also a glycosylated cationic dimer, and is sometimes referred to as vascular permeability factor (VPF). VEGF has diverse effects, depending on the specific biological context in which it is found. VEGF is a potent endothelial cell mitogen, and directly contributes to induction of angiogenesis in vivo by promoting endothelial cell growth during normal embryonic development, wound healing, and tissue regeneration/reorganisation. The VEGF proteins of the invention share the angiogenic and other properties of VEGF, but are distributed and expressed in tissues differently to VEGF. The proteins can therefore be used to accelerate angiogenesis in wound healing. Antibodies against the proteins can be used for inhibiting angiogenesis. The antibodies can also be used diagnostically to quantitatively detect VEGF-B. Primers complementary to the coding sequences for the proteins of the invention can also be used to detect VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy specimens may be useful as an indicator of metastatic risk. VEGF-B expression in a cell can be retarded using antisense sequences direct against the VEGF coding sequences, this is especially useful in retarding VEGF expression in tumour cells.
SQ Sequence 188 AA;

Query Match 100.0%; Score 121; DB 21; Length 188;

Best Local Similarity 100.0%; Pred. No. 6,06e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvqrcgccc 83
|||
QY 69 pscvtvqrcgccc 82

RESULT 9
ID W04827 standard; Protein: 195 AA.
AC W04827;
DT 28-APR-1997 (first entry)
DE Heart vascular endothelial growth factor-B174.
KW Endothelial cell; proliferation; vascular endothelial growth factor; VEGF; VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration; vascular permeability factor; cell mitogen; angiogenesis; cell growth; embryonic development; wound healing; tissue reorganisation; antibody; cancer; metastatic risk; tumour cell; mouse.
OS Mus musculus.
PN W09626736-A1.
PD 06-SEP-1996.
PF 01-MAR-1996; U02957.
PR 01-MAR-1995; US-397651.
PR 06-JUN-1995; US-469427.
PR 06-DEC-1995; US-569063.
PA (LUDM-) LUDWIG INST CANCER RES.
PI (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
DR WPI: 96-412582/41.
DR N-PSDB: T37911.
PT Vascular endothelial growth factor VEGF-B proteins - useful to accelerate angiogenesis in wound healing, also related nucleic acid and antibodies for cancer diagnosis.
PS Claim 18: Page 56-57; 107pp; English.
CC W04824-W04831 represent the vascular endothelial growth factor (VEGF) proteins of the invention, which promote endothelial or mesodermal cell proliferation. VEGF is also a glycosylated cationic dimer, and is sometimes referred to as vascular permeability factor (VPF). VEGF has diverse effects, depending on the specific biological context in which it is found. VEGF is a potent endothelial cell mitogen, and directly contributes to induction of angiogenesis in vivo by promoting endothelial cell growth during normal embryonic development, wound healing, and tissue regeneration/reorganisation. The VEGF proteins of the invention share the angiogenic and other properties of VEGF, but are distributed and expressed in tissues differently to VEGF. The proteins can therefore be used to accelerate angiogenesis in wound healing. Antibodies against the proteins can be used for inhibiting angiogenesis. The antibodies can also be used diagnostically to quantitatively detect VEGF-B. Primers complementary to the coding sequences for the proteins of the invention can also be used to detect VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy specimens may be useful as an indicator of metastatic risk. VEGF-B expression in a cell can be retarded using antisense sequences direct against the VEGF coding sequences, this is especially useful in retarding VEGF expression in tumour cells.
SQ Sequence 195 AA;

Query Match 100.0%; Score 121; DB 21; Length 195;
Best Local Similarity 100.0%; Pred. No. 6,06e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvqrcgccc 83
|||
QY 69 pscvtvqrcgccc 82

RESULT 10
ID W00863 standard; Protein: 207 AA.
AC W00863;
DT 30-NOV-1996 (first entry)
DE Murine VRF186.
KW VRF; vascular endothelial growth factor; VEGF; SOM175; neuron; astroglial proliferation.
OS Mus musculus.

FH Key Location/Qualifiers
 FT Peptide 1..21
 PN /label= sig_peptide
 MO627007-A1.
 PD 06-SEP-1996.
 PF 22-FEB-1996: AU0094.
 PR 02-MAR-1995: AU-001457.
 PR 20-NOV-1995: AU-006647.
 PR 22-DEC-1995: AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M.
 PI Weber G.
 DR WPI: 96-412774/41.
 DR N-PSDB: T13809.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival.
 PS Example 5: Fig 9: 113pp: English.
 CC VRF186 (W00863) is the murine homologue of human vascular endothelial
 CC growth factor-like polypeptide SOM175 (W00725), a protein capable of
 CC inducing astroglial proliferation and of promoting neural survival
 CC and/or proliferation. Its amino acid sequence was deduced from a
 CC cDNA clone (T13809) isolated from a new-born mouse brain cDNA
 CC library. An alternatively spliced variant, VRF189 (W00864), was
 CC also identified.
 SQ Sequence 207 AA;

Query Match 100.0%; Score 121; DB 19; Length 207;
 Best Local Similarity 100.0%; Pred. No. 6.06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvgrcgccp 83
 |||||||
 Qy 69 PSCVTVGRCGCCP 82

RESULT 11
 ID W00725 standard; Protein: 207 AA.
 AC W00725:
 DT 30-NOV-1996 (first entry)
 DE Vascular endothelial growth factor-like protein SOM175.
 KW Vascular endothelial growth factor; VEGF; VEGF185; SOM175; neuron;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..21
 PN /label= sig_peptide
 MO627007-A1.
 PD 06-SEP-1996.
 PF 22-FEB-1996: AU0094.
 PR 02-MAR-1995: AU-001457.
 PR 20-NOV-1995: AU-006647.
 PR 22-DEC-1995: AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M.
 PI Weber G.
 DR WPI: 96-412774/41.
 DR N-PSDB: T13610.
 PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival.
 PS Claim 11: Page 41: 113pp: English.
 CC Human vascular endothelial growth factor (VEGF)-like polypeptide
 CC (W00725) is capable inducing the proliferation of vascular
 CC endothelial cells, of interacting with flt-1/Flk-1 receptors,
 CC and of inducing cell migration, cell survival and/or an increase
 CC in intracellular levels of alkaline phosphatase. It shows 33.3%
 CC identity with human VEGF (see also W00724). Splice variants
 CC (W00726-28) of SOM175 have also been identified. Recombinant SOM175
 CC can be produced in host cells transformed with vectors carrying
 CC SOM175 cDNA (see also T13610). It is useful for inducing astroglial
 CC proliferation and for promoting neural survival and/or proliferation.
 SQ Sequence 207 AA;

Query Match 100.0%; Score 121; DB 19; Length 207;
 Best Local Similarity 100.0%; Pred. No. 6.06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvgrcgccp 83
 |||||||
 Qy 69 PSCVTVGRCGCCP 82

RESULT 12
 ID W04831 standard; Protein: 207 AA.
 AC W04831:
 DT 28-APR-1997 (first entry)
 DE Vascular endothelial growth factor-B186.
 KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse.
 OS Homo sapiens.
 PN W0626736-A1.
 PD 06-SEP-1996.
 PF 01-MAR-1996: U02957.
 PR 01-MAR-1995: US-397651.
 PR 06-JUN-1995: US-469427.
 PR 06-DEC-1995: US-569063.
 PA (LUDWIG-) LUDWIG INST CANCER RES.
 PA (VYHE-) UNIV HELSINKI LICENSING LTD OY.
 PI Aitalo K, Eriksson U, Oloisson B, Pajusola K;
 PI WPI: 96-412582/41.
 DR N-PSDB: T137915.
 DR WPI: 96-412582/41.
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis
 PS Claim 18: Page 62: 107pp: English.
 CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
 CC proteins of the invention, which promote endothelial or mesodermal cell
 CC proliferation. VEGF is also a glycosylated cationic dimer, and is
 CC sometimes referred to as vascular permeability factor (VPF). VEGF has
 CC diverse effects, depending on the specific biological context in which it
 CC is found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting endothelial
 CC cell growth during normal embryonic development, wound healing, and
 CC tissue regeneration/reorganisation. The VEGF proteins of the invention
 CC share the angiogenic and other properties of VEGF, but are distributed
 CC and expressed in tissues differently to VEGF. The proteins can therefore
 CC be used to accelerate angiogenesis in wound healing. Antibodies against
 CC the proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences directed against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.
 SQ Sequence 207 AA;

Query Match 100.0%; Score 121; DB 21; Length 207;
 Best Local Similarity 100.0%; Pred. No. 6.06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 pscvtvgrcgccp 83
 |||||||
 Qy 69 PSCVTVGRCGCCP 82

RESULT 13
 ID W04830 standard; Protein: 207 AA.
 AC W04830:
 DT 28-APR-1997 (first entry)
 DE Vascular endothelial growth factor-B186.
 KW Endothelial cell; proliferation; vascular endothelial growth factor; VPF;
 KW VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse.
 OS Homo sapiens.
 PN W0626736-A1.
 PD 06-SEP-1996.
 PF 01-MAR-1996: U02957.
 PR 01-MAR-1995: US-397651.
 PR 06-JUN-1995: US-469427.
 PR 06-DEC-1995: US-569063.
 PA (LUDWIG-) LUDWIG INST CANCER RES.
 PA (VYHE-) UNIV HELSINKI LICENSING LTD OY.
 PI Aitalo K, Eriksson U, Oloisson B, Pajusola K;
 PI WPI: 96-412582/41.
 DR N-PSDB: T137915.
 DR WPI: 96-412582/41.
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis
 PS Claim 18: Page 62: 107pp: English.
 CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
 CC proteins of the invention, which promote endothelial or mesodermal cell
 CC proliferation. VEGF is also a glycosylated cationic dimer, and is
 CC sometimes referred to as vascular permeability factor (VPF). VEGF has
 CC diverse effects, depending on the specific biological context in which it
 CC is found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting endothelial
 CC cell growth during normal embryonic development, wound healing, and
 CC tissue regeneration/reorganisation. The VEGF proteins of the invention
 CC share the angiogenic and other properties of VEGF, but are distributed
 CC and expressed in tissues differently to VEGF. The proteins can therefore
 CC be used to accelerate angiogenesis in wound healing. Antibodies against
 CC the proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences directed against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.
 SQ Sequence 207 AA;

KW VEGF: endothelium; mesodermal cell; cationic dimer; tissue regeneration;
 KW vascular permeability factor; cell mitogen; angiogenesis; cell growth;
 KW embryonic development; wound healing; tissue reorganisation; antibody;
 KW cancer; metastatic risk; tumour cell; mouse.
 OS Mus musculus.
 PD WO662736-A1.
 PD 06-SEP-1996.
 PR 01-MAR-1996: U02957.
 PR 01-MAR-1995: US-397651.
 PR 06-JUN-1995: US-469427.
 PR 06-DEC-1995: US-569063.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIT HELSINKI LICENSING LTD OY.
 PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
 DR WPI: 96-412582/41.
 DR N-PSDB: T37914.
 PT Vascular endothelial growth factor VEGF-B proteins - useful to
 PT accelerate angiogenesis in wound healing, also related nucleic acid
 PT and antibodies for cancer diagnosis.
 PS Claim 18: Page 60-61: 107pp: English.
 CC W04824-W04831 represent the vascular endothelial growth factor (VEGF)
 CC proteins of the invention, which promote endothelial or mesodermal cell
 CC proliferation. VEGF is also a glycosylated cationic dimer, and is
 CC sometimes referred to as vascular permeability factor (VPF). VEGF has
 CC diverse effects, depending on the specific biological context in which it
 CC is found. VEGF is a potent endothelial cell mitogen, and directly
 CC contributes to induction of angiogenesis in vivo by promoting endothelial
 CC cell growth during normal embryonic development, wound healing, and
 CC tissue regeneration/reorganisation. The VEGF proteins of the invention
 CC have the angiogenic and other properties of VEGF, but are distributed
 CC and expressed in tissues differently to VEGF. The proteins can therefore
 CC be used to accelerate angiogenesis in wound healing. Antibodies against
 CC the proteins can be used for inhibiting angiogenesis. The antibodies can
 CC also be used diagnostically to quantitatively detect VEGF-B. Primers
 CC complementary to the coding sequences for the proteins of the invention
 CC can also be used to detect VEGF-B coding sequences. Quantification of
 CC VEGF-B in cancer biopsy specimens may be useful as an indicator of
 CC metastatic risk. VEGF-B expression in a cell can be retarded using
 CC antisense sequences direct against the VEGF coding sequences, this is
 CC especially useful in retarding VEGF expression in tumour cells.
 SQ Sequence 207 AA.

Query Match 100.0%; Score 121; DB 21; Length 207;
 Best Local Similarity 100.0%; Pred. No. 6,06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 70 pscvtvrggccc 83
 OY 69 pscvtvrggccc 82

RESULT 14
 ID W07611 standard; Protein: 221 AA.
 AC W07611:
 DT 01-SEP-1997 (first entry)
 DE Human vascular endothelial growth factor 3.
 KW Human vascular endothelial growth factor; hVEGF3; angiogenesis;
 KW tumour; inflammation; rheumatoid arthritis; diabetic retinopathy;
 KW psoriasis; bone; periodontium; ligament; antagonist.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT 69..82
 FT /label= PDGF/VEGF_family_signature
 FT /note="conserved PXCXXKXRCGCCN motif"
 PN WO639421-A1.
 PD 12-DEC-1996.
 PD 06-JUN-1995: U07283.
 PR 06-JUN-1995: WO-07283.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Olsen H, Rosen CA, Hu JS;
 DR WPI: 97-043056/04.
 DR N-PSDB: T44071.
 PT DNA encoding human vascular endothelial growth factor 3 - useful to

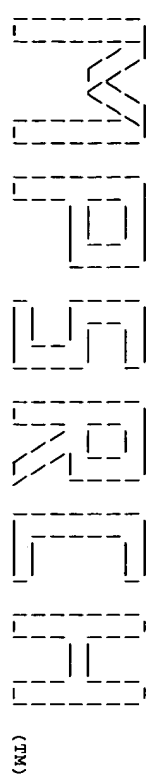
PT develop prods. for, e.g. stimulating angiogenesis or treating
 PT tumours, inflammation or rheumatoid arthritis
 PS Claim 11: Page 44: 56pp: English.
 CC This sequence is that of human vascular endothelial growth factor 3
 CC (VEGF3). The growth factor can be used to stimulate angiogenesis and
 CC wound healing, and to promote vascular tissue repair. It can also be
 CC used to induce the growth of damaged bone, periodontium or ligament
 CC tissue. VEGF3 antagonists can be used to inhibit tumour growth, or to
 CC treat diabetic retinopathy, inflammation, rheumatoid arthritis or
 CC psoriasis. VEGF3 is structurally related to the PDGF/VEGF family
 CC and it includes the conserved signature motif for the family (see
 CC features table).
 SQ Sequence 221 AA.

Query Match 100.0%; Score 121; DB 23; Length 221;
 Best Local Similarity 100.0%; Pred. No. 6,06e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 69 pscvtvrggccc 82
 OY 69 pscvtvrggccc 82

RESULT 15
 ID W14894 standard; Protein: 620 AA.
 AC W14894:
 DT 05-JUL-1997 (first entry)
 DE Human c-Fos induced growth factor (clone HF175 ORF2 product).
 KW c-Fos induced growth factor; FGF; Fos regulated gene;
 KW proto-oncogene; lung disorder; cancer; tumour; therapy;
 KW antibody; transgenic animal.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT misc_difference 16
 FT /note="residue 16 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"
 FT misc_difference 26
 FT /note="residue 26 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"
 FT misc_difference 29
 FT /note="residue 29 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"
 FT misc_difference 47
 FT /note="residue 47 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"
 FT misc_difference 71
 FT /note="residue 71 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"
 FT misc_difference 72
 FT /note="residue 72 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"
 FT misc_difference 76
 FT /note="residue 76 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"
 FT misc_difference 136
 FT /note="residue translated from ORF2 of HF175
 FT is Ile"
 FT misc_difference 220
 FT /note="residue translated from ORF2 of HF175
 FT is Ile"
 FT misc_difference 341
 FT /note="residue translated from ORF2 of HF175
 FT is His"
 FT misc_difference 344
 FT /note="residue translated from ORF2 of HF175
 FT is Phe"
 FT misc_difference 377
 FT /note="residue translated from ORF2 of HF175
 FT is Phe"
 FT misc_difference 435
 FT /note="residue translated from ORF2 of HF175
 FT is Leu"
 FT misc_difference 486
 FT /note="residue 435 corresponds to an in-frame
 FT stop codon in reading frame 2 of HF175"

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Mparch_nun n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 1 11:43:00 1998; MasPar time 893.19 Seconds

Tabular output not generated. 1335.277 Million cell updates/sec

Title: >US-09-033-662-1
Description: (1-666) from US09033662.seq
Perfect Score: 666
N.A. Sequence: 1 ATGAGAGGTGTAGATAG.....GCCGAGCTGCGAGGTGA 666
Comp: TACTCTTCACATCTTATTC.....CGGCTTCGAGCTTCACAT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 2275026 segs, 895388244 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-est55
1:em-est1 2:em-gss1 3:em-gss2 4:em-gss3
Database: genbank-est107
5:gb-est1 6:gb-est10 7:gb-est11 8:gb-est12 9:gb-est13
10:gb-est14 11:gb-est15 12:gb-est16 13:gb-est17
14:gb-est18 15:gb-est19 16:gb-est20 17:gb-est21
18:gb-est22 19:gb-est23 20:gb-est24 21:gb-est25 22:gb-est26
23:gb-est27 24:gb-est28 25:gb-est29 26:gb-est30 27:gb-est31
28:gb-est32 29:gb-est33

Statistics: Mean 10.628; Variance 2.514; scale 4.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	401	60.2	445	8	AA292448	z129f01.r1 Soares ovar	0.00e+00
2	373	56.0	415	24	AA310070	EST180930 Jurkat T-cel	0.00e+00
3	282	43.8	531	6	AA434485	zw31a04.r1 Soares ovar	0.00e+00
4	253	38.0	389	18	AA174133	uc07p07.r1 Soares ovar	0.00e+00
5	221	33.2	341	16	H35905	yo54a11.r1 Homo sapien	0.00e+00
6	218	32.7	312	16	R90829	yn02g09.r1 Homo sapien	0.00e+00
7	209	31.4	491	16	AI155033	ub78b01.r1 Soares ovar	0.00e+00
8	192	28.8	410	17	AA117413	mm94g06.r1 Soares ovar	4.53e-273
9	161	24.2	423	23	AA073660	zn25g01.r1 Soares ovar	1.66e-219
10	154	23.1	553	21	AA082818	z447n01.r1 Soares ovar	1.68e-207
11	132	19.8	523	21	AA040843	zp36a04.r1 Soares ovar	4.88e-170
12	121	18.2	374	22	AA182397	mo61a06.r1 Soares ovar	1.68e-151
13	120	18.0	231	23	AA117672	mo61a06.r1 Soares ovar	8.00e-150

14	118	17.7	225	5	T08411	EST06302 Homo sapiens	1.80e-146
15	116	17.4	565	10	AA633535	np66d06.s1 NCI-CGAP_Br	4.00e-143
16	116	16.8	118	10	AA191903	ov51f06.r1 Soares ovar	1.90e-136
17	109	16.4	566	18	AA141331	ak08g12.s1 Soares ovar	1.86e-131
18	81	12.2	502	13	AA843655	ak08g12.s1 Soares ovar	1.08e-95
19	76	11.4	88	15	AA917955	0168h05.s1 NCI-CGAP_K1	1.00e-77
20	74	11.1	493	6	AA343459	zw31a04.s1 Soares ovar	1.47e-74
21	66	9.9	297	16	R88630	ym95c03.r1 Homo sapien	4.79e-63
22	66	9.9	381	12	AA073557	mm94h03.r1 Soares ovar	4.79e-63
23	63	9.5	490	12	AA741539	ob29c01.s1 NCI-CGAP_K1	2.02e-57
24	56	8.4	252	12	AA754459	97SN1787 Rice Immature	8.34e-47
25	56	8.4	252	12	AA754459	97SN1787 Rice Immature	8.34e-47
26	53	8.0	469	13	AA843530	ak08b11.s1 Soares ovar	2.42e-42
27	52	7.8	247	12	AA554458	97SN1784 Rice Immature	7.23e-41
28	51	7.7	210	7	AA510867	vh55d06.r1 Soares ovar	2.13e-35
29	48	7.2	247	12	AA754458	97SN1784 Rice Immature	4.85e-35
30	47	7.1	289	20	N87395	L3711F Fetal heart, La	1.33e-33
31	45	6.8	283	8	AA491141	aa48e07.r1 NCI-CGAP_GC	6.74e-31
32	43	6.5	281	8	AA252283	zs13b04.r1 NCI-CGAP_GC	6.04e-28
33	43	6.5	284	8	AA284431	zs59d08.r1 NCI-CGAP_GC	6.04e-28
34	43	6.5	301	8	AA252749	zs28b07.r1 NCI-CGAP_GC	6.04e-28
35	43	6.5	326	8	AA259024	zs35d11.r1 NCI-CGAP_GC	6.04e-28
36	43	6.5	426	8	AA465305	aa24b04.r1 NCI-CGAP_GC	6.04e-28
37	42	6.3	231	9	AA568606	nm21d08.s1 NCI-CGAP_CO	1.48e-26
38	41	6.2	171	13	AA809010	nv31e11.r1 NCI-CGAP_Br	3.56e-25
39	41	6.2	301	18	AA186160	qe45b11.r1 Soares ovar	3.56e-25
40	41	6.2	320	8	AA290917	zs44b05.r1 NCI-CGAP_GC	3.56e-25
41	40	6.0	149	11	AA703302	EST0002 Human Fetal Br	8.31e-24
42	40	6.0	321	11	AA663755	ae66f05.s1 Soares ovar	8.31e-24
43	39	5.9	285	10	AA612827	nq26h07.s1 NCI-CGAP_CO	1.89e-22
44	39	5.9	303	8	AA252684	zs26d02.r1 NCI-CGAP_CO	1.89e-22
45	39	5.9	611	14	AA799651	EST189148 Normalized r	1.89e-22

ALIGNMENTS

RESULT 1
LOCUS AA292448 445 bp mRNA EST 08-AUG-1997
DEFINITION z129f01.r1 Soares ovar tumor NBH07 Homo sapiens cDNA clone 723769
5' similar to TR:G1216396 G1216396 VEGF RELATED FACTOR ISORORM
VR186 PRECURSOR. ; mRNA sequence.

ACCESSION
AA292448
NID
KEYWORDS
SOURCE
ORGANISM

Homo sapiens
Eukaryota; Eukaryota; Eukaryota; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Catarrhini; Homidae;
Homo.

REFERENCE
1 (bases 1 to 445)
Hillier, L., Clark, N., Dubouche, J., Ellington, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, D., Rifkin, B., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.
WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lln.gov) for further information.
Insert Length: 941 Std Error: 0.00
Seq primer: -26ml3 rev2 EF from Amersham
High quality sequence stop: 425.
Location/Qualifiers
1. 445
/organism="Homo sapiens"
/note="Organ: Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1.0"

FEATURES
SOURCE

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae Homo.

1 (bases 1 to 531)

Hillier, L., Allen, M., Bowles, L., Dubnue, T., Geisel, G., Jost, S., Kucuba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theisling, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

WashU-Merck EST Project 1997

Unpublished (1997)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the IMAG Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence rev2: 470

1. .531

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/organism:Homo sapiens"
/notes:"Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - 019g(ct) primer (5'
TGTTACCATCTGGAAGGCGGCGCGCGGCTTTTCTTTTCTTTTCTTTTCTTTT
3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
J. Fatima Bonaldo."

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/cclone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/rissue_type="Ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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BASE COUNT	111 a	162 c	163 g	95 t
ORIGIN				

Query Match	43.88;	Score 292;	DB 6;	Length 531;
Best Local Similarity	98.78;	Pred. No. 0.00e+00;		
Matches 311;	Conservative 0;	Mismatches 1;	Indels 3;	Gaps 3

Db	11	GATGAAGGGGTCATGATGATAGATGTATATACTCGGCCATACCTGCAGGCCCGGAGAGT	70
Qy	93	CAGCAAAATGCTGTATGATGATGATGTATATACTCGGCCATACCTGCAGGCCCGGAGAGT	155
Db	71	GGTGTGCCCTTGACTGTGAGACTCATATGGCAGCGGTGGCCAAACAGCTGTGTGCCACGTG	136
Qy	153	GGTGTGCCCTTGACTGTGAGACTCATATGGCAGCGGTGGCCAAACAGCTGTGTGCCACGTG	212
Db	131	CGTACTGTGCAGCCCTGTGGTGCGCTGTGTCGCGTGCACATGAGCCGTGGAGTGTGTGCCAC	189
Qy	213	CGTACTGTGCAGCCCTGTGTGTGTGCTGTGCTGCCCTGTACATATGCGCTGTGAGTGTGTGCCAC	272
Db	130	TGGCAGCACCAAGTCCGAGATGCAGATCTCTCATGTATCCGGTATCCCGAGACTCAGTGGG	248

	RESULT	4	AII74I83	369 bp	mRNA	EST	07-OCT-1998
	LOCUS		uc07boj7.r1	Soares mouse mammary gland NBMG Mus musculus cDNA clone			
	DEFINITION		1397269 5' similar to SW:VEGB_MOUSE P49766 VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR ; , mRNA sequence.				

ACCESSION	A1174183
NTD	93720325
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
AUTHORS
Eutheria: Metazoa; Chordata; Vertebrata; Mammalia: Eutheria;
Rodentia: Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 389)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gelsel, S., Krcabee, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)

TITLE	EST PROJECT
THE WASHU-HHMI MOUSE JOURNAL	UNPUBLISHED (1996)

Contact: Marra M/Mouse EST Project
 Mashu-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel.: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:908985
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 378.
 Location/Qualifiers
 1..389

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/organism="Mus musculus"
/strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pT7n3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCATCTGTAAGTGGAGCGCCGCAGATGTTTTTTTTTTTTTCCTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7n3D-Pac
RNA provided by Dr. Minoru Ko, Wayne State Univ., Detroit,
constructed and normalized by Bento Soares and M. B. de
Bonaldo."
/db_xref="taxon:10090"
/clone="1397269"
/clone_1lb="Soares mouse mammary gland NBMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

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Query Match	38.0%;	Score 253;	DB 18;	Length 389;
Best Local Similarity	88.7%;	Pred. No. 0.00e+00;		
Matches	307;	Conservative	0;	Mismatches 36; Indels 3; Gaps 0;

Db	47	CCAGAGCCCCCTGTGTCGCCAGTTTATATGGCCCCACG-ACAGAGAAAGAGTGTGCATGGA	105
Qy	53	CCGAGGCCCTGTCTCTCCAGCCTTATGTGCCCTGGCCACCAAGAGAAAGTGTGTCAATGGA	112
Db	106	TAGACGTTTATGCAAGTGTCCACATATGCCAGCCAGAGGAGTGTGTGTCCTGTGCATGG	165
Qy	113	TAGATGTGTATACCTGCGCCTTACCTGTCCAGCCCCGGGAGGTGTGTGTCTCCCTTGA	172
Db	156	AACATCATGGGCAATGTGGTCAAAACATAGTGCCACAGCTGTGTACTGTGCACGGCTGTG	225
Qy	173	AGCTCATGGGCACCGTGGSCAAACAGCTGGTGGCCACTCGTGACTGTGTACAGCCTGTG	232
Db	226	GTGGCTGCTGCCCTGCAGCATGGCCTGGAATGTGTGCCACTGGCA-CAACAAATGCCGA	284
Qy	233	GTGGTGTCTGCCCTGCAGCATGGCCTGGAGTGTGTGCCACTGGGCGAGCAACAATGCCGA	292
Db	285	TGCAGATCCCTCATATCCAGTACCGGAGCATGAGTGTGGGGGAGATGTGC-TGGAGAAC	343
Qy	293	TGCAGATCTCTATATATCCGGTATCCCGAGCATGACGTGGGGGAGATGTCTCTTGGAAAGAC	352
Db	344	ACAGCCAAATGTGAATGCAGACCAAAAAAAGAGAGATGCTGTGAA	389
Qy	353	ACAGCCAGTGTGAATGCAGACCTAAAAAAGAGACATGCTGTGAA	398

	5					
RESULT	H39505	341 bp	mRNA	EST		16-AUG-1995
LOCUS	Y05441.1	r1 Homo sapiens cDNA clone 181724		5'		
DEFINITION	H39505					
ACCESSION	G915581					
NID						
KEYWORDS						
SOURCE	human clone=181724	library=Scares breast 3NbHst vector=D773				

SOURCE human clone-181/24 library-Soares breast 3BHBst vector-PT73D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13RP1 Rst6I-Not I Rst6I-Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGTAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTV73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Felima Bonaldo.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens					
Eukaryotae: Metazoa: Eumetazoa: Bilateria: Coelomata: Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes					
Sarcopterygii: Chonamata: Tetrapoda: Amniota: Mammalia: Theria: Eutheria: Archonta: Primates: Catarrhini: Homnidae: Homo: 1 (cases 1 to 341)					
Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.					
			The WashU-Merck EST Project		
			Unpublished (1995)		

FEATURES
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence drops: 314
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Location/Qualifiers

source	1. .341	/organism="Homo sapiens"	/clone="181724"	65 a	133 c	87 g	50 t	6 others
BASE COUNT								
ORIGIN								

Query Match	33.2%	Score 221	DB 161	Length 341
Best Local Similarity	96.0%	Pred. No. 0.00e+00		
Matches 243	Conservative	0	Mismatches 7	Indels 3
			Gaps	
Db	3	ACTCCCAACACGGGTCCCAAGCCCGTTCGTTCCGGGCTGGGACATCGCCCCGGAGC	32	
QY	415	ACTCCCAACACCG-TCCCAAGCCCGTTCGTTCCGGGCTGGGACTCGCCCCGGAGC	473	
Db	63	ACCCTCCCACTGATCATCACCA-TCCCACTCCAGCCCCAGGGCCCTCTGCCACGCTG	121	
QY	474	ACCCTCCCACTGATCATCACCAATCCCACTCCAGCCCCAGGGCCCTCTGCCACGCTG	533	
Db	122	CACCCAGANANACCAAGCGCCCTGACCCCGGACTGCCGCTGCCGCTGCCAGCCCGAG	181	
QY	534	CACCCAGACACCAAGTGCCTTGACCCCGGACTGCCGCTGCCGCTGCCAGCCCGAG	593	
Db	182	CTTCCTCCGTTGCCAAGG-GGGAGCTTAGAGCTCAACCCAGACCTCGCAGTCCCGAA	240	
QY	594	CTTCCTCCGTTGTAAGGGCGGGCTTAGAGCTCAACCCAGACCTCGCAGTCCCGAA	653	
Db	241	GCTCGGAAGGTGA 253		
QY	654	GCTCGGAAGGTGA 666		

LOCUS	6	312 bp	mRNA	EST	25-AUG-1995
DEFINITION	R90829				
ACCESSION	U020409.1		Homo sapiens cDNA clone 167296 5'.		
NID	R90829				
KEYWORDS	g958369				
SOURCE	EST.				
	humam clone=167296		library=Scars adult brain N244B55Y		

SOURCE
human clone-16/296 library-Soares adult brain N2b4H555Y vector-pT73D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-MJRp1 RstIte-Not I RstIte-Eco RI 55-year old male, 1st strand cDNA was primed with a Not I - oligo(dT) primer 15',
TGTCACATCTGAGTGGAGCGCGCGCTTTTTTTTTTTTTTT 31',
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library RNA was constructed by Bento Soares and M. Felicia Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla.

ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
Homo sapiens	1 (bases 1 to 312)	The Washu-Merck EST Project	Unpublished (1995)	
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kuehba,T., Le,M., Lennon,G., Merril,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaks,E., Waterston,R., Wallamson,A., Wohlmann,P. and Wilson,R.			

Contact: Wilson RK
WashU-Merck ESI Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: esi@watson.wustl.edu
High quality sequence stops: 207
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact lin

IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 378.

FEATURES

location/Qualifiers
1..553

/organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2 (Ntera-2/c1.D1) precursor cells induced with Retinoid Acid for 1 week, followed by 3 weeks in mitotic inhibitors (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 3' CTCGAGTCTTTTCTTTTCTTTT 3'."
/db_xref="taxon:9606"
/clone="548449"
/dev_stage="Ntera-2/RM-MT neuroepithelial cells"
/lab_host="SOLR (Kanamycin resistant)"

BASE COUNT 133 a 173 c 140 g 99 t 8 others

ORIGIN

Query Match 23.1%; Score 154; DB 11; Length 553;
Best Local Similarity 95.3%; Pred. No. 1,68e-207;
Matches 164; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Db 2 CCATCCACATCCAGAGCCGCTCTGCCAGCTGCACGACGACGACGACGACG 61

Qy 495 CCATCCACATCCAGAGCCGCTCTGCCAGCTGCACGACGACGACGACGACG 554

Db 62 TGACCCCGGACGCTGCGCTGCGCGAGCGCGGCGGCGGCGGCGGCGGCGG 120

Qy 555 TGACCCCGGACGCTGCGCTGCGCGAGCGCGGCGGCGGCGGCGGCGGCGG 614

Db 121 GGGCTTACGCTCAACCGACCTGCGAGTGGCGGAGCTGCGAGCTGA 172

Qy 615 GGGCTTACGCTCAACCGACCTGCGAGTGGCGGAGCTGCGAGCTGA 666

RESULT 11 AA040843 523 bp mRNA EST 30-AUG-1996

LOCUS 2447H01.F1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone

DEFINITION 466001 5', mRNA sequence.

ACCESSION AA040843

NID G1517139

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

AUTHORS Vertebata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 523)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Trevasaks, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

/note="Organ: uterus; Vector: pT7T3-Pac; Site.1: N. . .
Site.2: Eco RI; 1st strand cDNA was primed with a N. . .
Oligo(dt) primer [5'
AAGTGAAGATTCGCGCGGCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N. . .
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="486001"
/clone_lib="Soares pregnant uterus NBHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
<1..>523

BASE COUNT 123 a 155 c 136 g 100 t 9 others

ORIGIN

Query Match 19.8%; Score 132; DB 21; Length 523;
Best Local Similarity 95.9%; Pred. No. 4.84e-170;
Matches 141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 1 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 60

Qy 520 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 579

Db 61 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 119

Qy 580 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 639

Db 120 TGCAGGTGCCGGAAGCTGCGAAGTGA 146

Qy 640 TGCAGGTGCCGGAAGCTGCGAAGTGA 666

RESULT 12 AA182397 374 bp mRNA EST 07-JAN-1997

LOCUS 2P36A04.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 611502

DEFINITION 5' similar to TR:G1216398 G1216398 VEF RELATED FACTOR ISOFORM

ACCESSION AA182397

NID G1766080

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

AUTHORS Vertebata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 374)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

/note="Organ: uterus; Vector: pT7T3-Pac; Site.1: N. . .
Site.2: Eco RI; 1st strand cDNA was primed with a N. . .
Oligo(dt) primer [5'
AAGTGAAGATTCGCGCGGCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N. . .
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="486001"
/clone_lib="Soares pregnant uterus NBHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
<1..>523

BASE COUNT 123 a 155 c 136 g 100 t 9 others

ORIGIN

Query Match 19.8%; Score 132; DB 21; Length 523;
Best Local Similarity 95.9%; Pred. No. 4.84e-170;
Matches 141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 1 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 60

Qy 520 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 579

Db 61 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 119

Qy 580 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 639

Db 120 TGCAGGTGCCGGAAGCTGCGAAGTGA 146

Qy 640 TGCAGGTGCCGGAAGCTGCGAAGTGA 666

RESULT 12 AA182397 374 bp mRNA EST 07-JAN-1997

LOCUS 2P36A04.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 611502

DEFINITION 5' similar to TR:G1216398 G1216398 VEF RELATED FACTOR ISOFORM

ACCESSION AA182397

NID G1766080

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

AUTHORS Vertebata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 374)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

/note="Organ: uterus; Vector: pT7T3-Pac; Site.1: N. . .
Site.2: Eco RI; 1st strand cDNA was primed with a N. . .
Oligo(dt) primer [5'
AAGTGAAGATTCGCGCGGCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N. . .
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="486001"
/clone_lib="Soares pregnant uterus NBHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
<1..>523

BASE COUNT 123 a 155 c 136 g 100 t 9 others

ORIGIN

Query Match 19.8%; Score 132; DB 21; Length 523;
Best Local Similarity 95.9%; Pred. No. 4.84e-170;
Matches 141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 1 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 60

Qy 520 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 579

Db 61 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 119

Qy 580 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 639

Db 120 TGCAGGTGCCGGAAGCTGCGAAGTGA 146

Qy 640 TGCAGGTGCCGGAAGCTGCGAAGTGA 666

RESULT 12 AA182397 374 bp mRNA EST 07-JAN-1997

LOCUS 2P36A04.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 611502

DEFINITION 5' similar to TR:G1216398 G1216398 VEF RELATED FACTOR ISOFORM

ACCESSION AA182397

NID G1766080

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

AUTHORS Vertebata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 374)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

/note="Organ: uterus; Vector: pT7T3-Pac; Site.1: N. . .
Site.2: Eco RI; 1st strand cDNA was primed with a N. . .
Oligo(dt) primer [5'
AAGTGAAGATTCGCGCGGCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N. . .
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="486001"
/clone_lib="Soares pregnant uterus NBHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
<1..>523

BASE COUNT 123 a 155 c 136 g 100 t 9 others

ORIGIN

Query Match 19.8%; Score 132; DB 21; Length 523;
Best Local Similarity 95.9%; Pred. No. 4.84e-170;
Matches 141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 1 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 60

Qy 520 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 579

Db 61 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 119

Qy 580 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 639

Db 120 TGCAGGTGCCGGAAGCTGCGAAGTGA 146

Qy 640 TGCAGGTGCCGGAAGCTGCGAAGTGA 666

RESULT 12 AA182397 374 bp mRNA EST 07-JAN-1997

LOCUS 2P36A04.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 611502

DEFINITION 5' similar to TR:G1216398 G1216398 VEF RELATED FACTOR ISOFORM

ACCESSION AA182397

NID G1766080

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

AUTHORS Vertebata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 374)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

/note="Organ: uterus; Vector: pT7T3-Pac; Site.1: N. . .
Site.2: Eco RI; 1st strand cDNA was primed with a N. . .
Oligo(dt) primer [5'
AAGTGAAGATTCGCGCGGCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N. . .
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="486001"
/clone_lib="Soares pregnant uterus NBHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
<1..>523

BASE COUNT 123 a 155 c 136 g 100 t 9 others

ORIGIN

Query Match 19.8%; Score 132; DB 21; Length 523;
Best Local Similarity 95.9%; Pred. No. 4.84e-170;
Matches 141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 1 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 60

Qy 520 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 579

Db 61 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 119

Qy 580 TGCGAGCGCGGAGCTCTCCGCTTGCAGAGN-GGGGCTTACGCTCAACCGACGACG 639

Db 120 TGCAGGTGCCGGAAGCTGCGAAGTGA 146

Qy 640 TGCAGGTGCCGGAAGCTGCGAAGTGA 666

RESULT 12 AA182397 374 bp mRNA EST 07-JAN-1997

LOCUS 2P36A04.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 611502

DEFINITION 5' similar to TR:G1216398 G1216398 VEF RELATED FACTOR ISOFORM

ACCESSION AA182397

NID G1766080

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

AUTHORS Vertebata; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 374)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

/note="Organ: uterus; Vector: pT7T3-Pac; Site.1: N. . .
Site.2: Eco RI; 1st strand cDNA was primed with a N. . .
Oligo(dt) primer [5'
AAGTGAAGATTCGCGCGGCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N. . .
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="486001"
/clone_lib="Soares pregnant uterus NBHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
<1..>523

BASE COUNT 123 a 155 c 136 g 100 t 9 others

ORIGIN

Query Match 19.8%; Score 132; DB 21; Length 523;
Best Local Similarity 95.9%; Pred. No. 4.84e-170;
Matches 141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 1 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 60

Qy 520 CTCTGCCNACGCTGACCCAGACACGACGACGACGACGACGACGACGACG 579

Db 61 TGCGAGCGCGGAGCTCTCC

DEFINITION np66406.s1 NCI-CGAP-Br2 Homo sapiens CDNA clone IMAGE:1131275
 Similar to IR:G1216398 G1216398 VEGF RELATED FACTOR ISOFORM VRF167
 PRECURSOR ; mRNA sequence.
 ACCESSION AA633535
 NID 92555395
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 565)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LML at:
www.bio.lml.gov/db/brp/image/image.html
 Insert Length: 648 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 411.
 Location/Qualifiers
 1..565
 /organism="Homo sapiens"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -
 o1190(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT7T3
 vector. This library is the normalized version of
 NCI-CGAP-Br1.1. Library was constructed by Bento Soares
 and M. Fatima Bonaldo."
 /db_xref="taxon:9606"
 /clone_image="IMAGE:1131275"
 /clone_1lb="NCI-CGAP-Br2"
 /sex="female, pooled"
 /tissue_type="breast"
 /lab_host="DH10B"
 /lab_host="DH10B"
 BASE COUNT 103 a 146 c 166 g 150 t
 ORIGIN
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 Best Local Similarity 91.4%; Pred. No. 4,00e-143;
 Matches 128; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Db 419 TCACCTCGAGCTCGGACCTGAGGTGCTGAGCTTAAGCCTGCGCTTG 478
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Cp 666 TCACCTTCGAGCTTCGGACCTGCGAGTGTGGGTGCTTAAGCCCGCCTTG 607
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 479 GCAACGAGAGAACTCGCGCTCGGACGAGTACAGATCCGGGGTCAAGGGCCTT 538
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Cp 606 ACAACGAGAGAGTGTGGGGTGCACAGCGGACGAGTCCGGGGTCAAGGGCACTG 547
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 539 GTGCTCTGGTGCAGCGCTG 558
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Cp 546 GTGCTCTGGTGCAGCGCTG 527
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: Tue Dec 1 12:22:18 1998
 Job time : 2358 secs.

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 WISENTH (TM)

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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 1 12:22:37 1998; Maspar time 99.63 Seconds

Tabular output not generated. 909.455 Million cell updates/sec

Title: >US-09-033-662-1
 Description: (1-666) From US09033662.seq
 Perfect Score: 666
 N.A. Sequence: 1 ATGACAGAGGTGAGATATAG.....GCCGAGAGCTGCGAGGTGA 666
 Comp: TACTCTTCACATCTATTTC.....GGCGCTTGAGAGCTTCACAT

Scoring table: TABLE default
 Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: n-genes32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39 40:part40

Statistics: Mean 8.606; Variance 5.714; scale 1.506

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description	Pred. No.
1	666	100.0	666	31	Human vascular endoth	0.00e+00
2	604	90.7	1094	23	Vascular endothelial	0.00e+00
3	558	83.8	624	28	VEGF-B166 coding sequ	0.00e+00
4	483	72.5	1242	23	Murine VRF186 CDNA	1.74e-285
5	445	66.8	624	28	VEGF-B166 coding sequ	4.71e-261
6	360	54.1	570	28	Fibrosarcoma VEGF-B16	6.49e-206
7	359	53.9	858	23	Vascular endothelial	2.83e-205
8	338	43.2	993	23	Vascular endothelial	1.29e-160
9	288	43.2	910	23	Vascular endothelial	1.05e-158
10	285	42.8	565	28	Adult heart VEGF-B167	3.66e-156
11	281	42.2	1141	23	Murine VRF167 CDNA	9.87e-145
12	263	39.5	405	28	VEGF-B12 coding sequ	8.55e-131
13	241	36.2	886	28	Partial VEGF-B coding	

ID	Score	Query Match	Length DB	ID	Description	Pred. No.
14	183	27.5	591	28	Adult heart VEGF-B174	2.78e-94
15	48	7.2	366	2	Human vascular endoth	7.17e-13
16	48	7.2	467	22	VEGF121 Cys+4 coding	7.17e-13
17	48	7.2	473	17	CDNA encoding human v	7.17e-13
18	48	7.2	498	2	Human vascular endoth	7.17e-13
19	48	7.2	576	37	Human vascular endoth	7.17e-13
20	48	7.2	599	22	VEGF165 Cys+4 coding	7.17e-13
21	48	7.2	605	17	CDNA encoding human v	7.17e-13
22	48	7.2	649	23	Vascular endothelial	7.17e-13
23	48	7.2	774	36	Human vascular endoth	7.17e-13
24	48	7.2	774	33	Human vascular endoth	7.17e-13
25	48	7.2	774	33	Antisense inhibitory	7.17e-13
26	48	7.2	774	39	Vascular endothelial	7.17e-13
27	48	7.2	774	39	Human vascular endoth	7.17e-13
28	48	7.2	1167	2	SAP(G14Ser)VEGF121 c	7.17e-13
29	48	7.2	1195	1	Human vascular ptema	7.17e-13
30	48	7.2	1220	22	SAP(G14Ser)4VEGF121	7.17e-13
31	48	7.2	1286	22	SAP-AlaMet-VEGF165 co	7.17e-13
32	48	7.2	1357	40	VEGF165-AlaMet-VEGF165	7.17e-13
33	48	7.2	1557	22	SAP(G14Ser)VEGF121(G	7.17e-13
34	48	7.2	1559	22	SAP-AlaMet-VEGF121(G1	7.17e-13
35	48	7.2	1649	37	DNA for VEGF/CPG2 fus	7.17e-13
36	48	7.2	1664	37	DNA for VEGF/CPG2 fus	7.17e-13
37	48	7.2	1787	37	DNA for VEGF/CPG2 fus	7.17e-13
38	48	7.2	1787	22	SAP-AlaMet-VEGF165-G1	7.17e-13
39	48	7.2	1790	37	DNA for VEGF/CPG2 fus	7.17e-13
40	48	7.2	1790	37	DNA for VEGF/CPG2 fus	7.17e-13
41	48	7.2	1802	22	SAP-AlaMet-VEGF165(G1	7.17e-13
42	48	7.2	1823	22	SAP-AlaMet-VEGF165(G1	7.17e-13
43	48	7.2	1832	37	DNA for VEGF/CPG2 fus	7.17e-13
44	48	7.2	1859	22	SAP(G14Ser)2VEGF165(7.17e-13
45	48	7.2	1873	39	Human vascular endoth	7.17e-13

ALIGNMENTS

RESULT 1
 ID T44071 standard; cDNA; 666 BP.
 AC T44071:
 DT 01-SEP-1997 (first entry)
 DE Human vascular endothelial growth factor 3 cDNA.
 KW Human vascular endothelial growth factor; hVEGF3; angiogenesis;
 KM tumour; inflammation; rheumatoid arthritis; diabetic retinopathy;
 OS psoriasis; bone; periodontium; ligament; antagonist; ss.
 OS Homo sapiens.
 FH Homo sapiens.
 FT Key Location/Qualifiers
 FT cds 1..666
 FT /tag= a
 FT /product= VEGF3
 FT MO639421-A1.
 FT 12-DEC-1996.
 PD 06-JUN-1995; U07283.
 PF 06-JUN-1995; U07283.
 PR 06-JUN-1995; WO-007283.
 PA (HOMA-) HUMAN GENOME SCI INC.
 PI Olsen H, Rosen CA, Hu JS;
 DR WPI: 97-043056/04.
 DR P-PSDB: W07611.
 PT DNA encoding human vascular endothelial growth factor 3 - useful for
 PT develop prods. for, e.g. stimulating angiogenesis or treating
 PT tumours, inflammation or rheumatoid arthritis
 PS Claim 1; Page 43; 56pp; English.
 CC This sequence encodes human vascular endothelial growth factor 3
 CC (VEGF3). The growth factor can be used to stimulate angiogenesis and
 CC wound healing, and to promote vascular tissue repair. It can also be
 CC used to induce the growth of damaged bone, periodontium or ligament
 CC tissue. VEGF3 antagonists can be used to inhibit tumour growth, or to
 CC treat diabetic retinopathy, inflammation, rheumatoid arthritis or
 CC psoriasis.
 SO Sequence 666 BP; 125 A; 232 C; 198 G; 111 T;

Query Match 100.0%; Score 666; DB 31; Length 666;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	53	CCGAGGCCCCGTGTCCTCCAGCCTGATGTCCTCCCTG66CACCAGAGAAAGTGTGTCATGGA	112
Db	281	tagagcttattatgacgtggtccacatgacacgccagggaggtgtgtgtcctctgacatg	340
Oy	113	TAGATGTGTATACTCGGCGTACCTGCGACGCCGGGGAGTGTGTGGTCCCTTGACTGTGG	172
Db	341	aactcatgaggaaatgtgtgtcaaaaactagtgccacagctgtgtgactgtgagagccttg	400
Oy	173	AGCTGATGAGGACCGGTGGCCAAACAGCTGTGTGCCACAGCTGCGTGTGATGTGCGACCTGTG	232
Db	401	gtggctgtctgcctcagatgagtcctgtgaaatgtgtgccactggtggaacaacaagctcgaa	460
Oy	233	GTGGGTGTGTCCTGAGAGATGTGGCTGGAGTGTGTGCCACTGGGACGACCAAGTCCGA	292
Db	461	tgcagatctctcaatgacccagtaaccgagacagctagctgtggtggagatgtctctgtgagaac	520
Oy	293	TGCAGATCTCTCATATATCCGATCCCGAGCTAGTCAGCTGGGGGAGTGTCTCTGGAAAGAC	352
Db	521	aacagccaatgtgaatgacacctaataaaagaagaagtctgtgaggtccagaacaagtgtg	580
Oy	333	ACAGCCAGTGTGAATGCGAGACTTAAAAAAGACAGTGTGTGAAGCCAGCAGAGGCTG	412
Db	581	ccatacaccacacacacgcgtcccccagccccgcctctgtccgggtctggaacttacccggag	640
Oy	413	CTAGCTCCGACACACACGTCGCCAGGCCCGCTTCTTCGGGGTGGAGACTGTGCCCGCCGAG	472
Db	641	cacctctccagactgtacatatca-tccactccagccccagagatcctctgcgcgctt	699
Oy	473	CACCTCTCCCGAGCTGACATCACCAATCCACATCCACGCCACAGCCCTCTCCACGCT	532
Db	700	gcacccacggcgccgaacgcctctgacccccggagacctgtgcgctgtlaagccgcgc	759
Oy	533	GCACCCAGCACACACAGTGCCTGTACCCCGGAGCTGCGCTGCTGTCAACCCGCA	592
Db	760	gtctctccatgtcccaaggcggtctlaagatccaacacagacactgtagtgcga	819
Oy	593	GCTTCTCTCCGTGTGTCAGAGGGCGGCGCTTAAGTCTCAACCCAGCACTCTCAGTGC CGGA	652
Db	820	agccgcgaagaatga	833
Oy	653	AGCTGCGAGAGCTGA	666

KW cancer: metastatic risk: tumour cell; mouse; ss.
OS Homo sapiens.
PN W09626736-A1.
PD 06-SEP-1996.
PF 01-MAR-1996: U02957.
PR 01-MAR-1995: US-397651.
PR 06-JUN-1995: US-469427.
PR 06-DEC-1995: US-569063.
PA (LUDM-) LUDMIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alitalo K, Eriksson U, Olofsson B, Pajusola K;
DR WPI: 96-412582/41.
DR P-PSDB: W04829.
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
PS Claim 1: Page 58-59; 107pp; English.
CC T37909-T37915 represent the coding sequences for the vascular endothelial
CC growth factor (VEGF) proteins of the invention, which promote endothelial
CC or mesodermal cell proliferation. VEGF is also a glycosylated cationic
CC dimer, and is sometimes referred to as vascular permeability factor
CC (VPF). VEGF has diverse effects, depending on the specific biological
CC context in which it is found. VEGF is a potent endothelial cell mitogen,
CC and directly contributes to induction of angiogenesis in vivo by
CC promoting endothelial cell growth during normal embryonic development,
CC wound healing, and tissue regeneration/reorganisation. The VEGF proteins
CC are distributed and expressed in tissues differently to VEGF. The
CC proteins can therefore be used to accelerate angiogenesis in wound
CC healing. Antibodies against the proteins can be used for inhibiting
CC angiogenesis. The antibodies can also be used diagnostically to
CC quantitatively detect VEGF-B. Primers complementary to the coding
CC sequences for the proteins of the invention can also be used to detect
CC VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy
CC specimens may be useful as an indicator of metastatic risk. VEGF-B
CC expression in a cell can be retarded using antisense sequences direct
CC against the VEGF coding sequences, this is especially useful in retarding
CC VEGF expression in tumour cells.
SQ Sequence 570 BP; 105 A; 198 C; 173 G; 94 T;

Query Match 54.1%; Score 360; DB 28; Length 570;

Best Local Similarity 100.0%; Pred. No. 1,49e-206;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 54 ccccgcccaaggccctgtctccaccgtatgctccctgagccagagaaagtgtgtc 113
OY 48 ccccgcccaaggccctgtctccaccgtatgctccctgagccagagaaagtgtgtc 107

DB 114 atggatagatgtgtatctacgtcgctacgtccagcccgaggagtggtgtcccttgac 173
OY 108 atggatagatgtgtatctacgtcgctacgtccagcccgaggagtggtgtcccttgac 167

DB 174 tctggagccatctatggtgacacgtgtgctgagccagctggtgtgctgtgacgcg 233
OY 168 tctggagccatctatggtgacacgtgtgctgagccagctggtgtgctgtgacgcg 227

DB 234 cttgtgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgac 293
OY 228 cttgtgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgac 287

DB 294 ccgagatgcagatccctatgataccgtgacccagacagctcaagctggtgtgagagctgtgac 353
OY 288 ccgagatgcagatccctatgataccgtgacccagacagctcaagctggtgtgagagctgtgac 347

DB 354 agaacacacagcagctgtgatacgcagacctaataaagagagacagctgtgtgagccagacag 413
OY 348 agaacacacagcagctgtgatacgcagacctaataaagagagacagctgtgtgagccagacag 407
```

RESULT 7

ID T33612 standard: cDNA: 858 BP.

AC T33612:

DT 30-NOV-1996 (first entry)

DE Vascular endothelial growth factor-like protein SOM175-e6+e7 cDNA.
KW Vascular endothelial growth factor; VEGF; SOM175-e6+e7; neuron;
OS Homo sapiens.
PN W09626736-A1.
PD 06-SEP-1996.
PF 22-FEB-1996: AU0094.
PR 02-MAR-1995: AU-001457.
PR 20-NOV-1995: AU-006647.
PR 22-DEC-1995: AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PA Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI: 96-412774/41.
DR P-PSDB: W00727.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Example 3: Page 44-45; 113pp; English.
CC 3 cDNA clones (T33611-13) code for splice variants (W00726-28)
CC of the human vascular endothelial growth factor-like polypeptide
CC SOM175 (see also W00725). They were identified in a human foetal
CC spleen library and respectively lack exon 6, exons 6+7, and exon 4
CC of the SOM175 gene (see also T33610). The cDNA clones can be
CC used to produce recombinant SOM175 proteins that are useful for
CC inducing astroglial proliferation and for promoting neural survival
CC and/or proliferation.
SQ Sequence 858 BP; 210 A; 243 C; 246 G; 159 T;

Query Match 53.9%; Score 359; DB 23; Length 858;

Best Local Similarity 99.7%; Pred. No. 6,49e-206;

Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
DB 53 ccccgcccaaggccctgtctccaccgtatgctccctgagccagagaaagtgtgtc 112
OY 48 ccccgcccaaggccctgtctccaccgtatgctccctgagccagagaaagtgtgtc 107

DB 113 atggatagatgtgtatctacgtcgctacgtccagcccgaggagtggtgtcccttgac 172
OY 108 atggatagatgtgtatctacgtcgctacgtccagcccgaggagtggtgtcccttgac 167

DB 173 tctggagccatctatggtgacacgtgtgctgagccagctggtgtgctgtgacgcg 232
OY 168 tctggagccatctatggtgacacgtgtgctgagccagctggtgtgctgtgacgcg 227

DB 233 cttgtgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgac 292
OY 228 cttgtgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgac 287

DB 293 ccgagatgcagatccctatgataccgtgacccagacagctcaagctggtgtgagagctgtgac 352
OY 288 ccgagatgcagatccctatgataccgtgacccagacagctcaagctggtgtgagagctgtgac 347

DB 353 agaacacacagcagctgtgatacgcagacctaataaagagacagctgtgtgagccagatag 412
OY 348 agaacacacagcagctgtgatacgcagacctaataaagagacagctgtgtgagccagatag 407

DB 413 g 413
OY 408 g 408
```

RESULT 8

ID T33611 standard: cDNA: 993 BP.

AC T33611:

DT 30-NOV-1996 (first entry)

ID	Accession	Location/Qualifiers
DE	Vascular endothelial growth factor-like protein SOM175-e6 cDNA.	
DE	Vascular endothelial growth factor; VEGF; SOM175-e6; neuron.	
KM	astroglial proliferation; ss.	
OS	Homo sapiens.	
FS	Key	
FT	Key	Location/Qualifiers
FT	cds	3..569
FT	cds	/*tag= a
FT	signal_peptide	3..65
FT	mat_peptide	/*tag= b
FT	mat_peptide	66..566
FT	mat_peptide	/*tag= c
PN	W09627007-A1.	
PD	06-SEP-1996.	
PE	22-FEB-1996.	
PR	02-MAR-1995; AU-001457.	
PR	20-NOV-1995; AU-006647.	
PR	22-DEC-1995; AU-007274.	
PA	(AMRA) - AMRAD OPERATIONS PVTY LTD.	
PI	Grimmond S, Hayward NK, Larsson C, Nordenskjold M;	
PI	Weber G;	
DR	WPI: 96-412774/41.	
P	P-PDB: W00726.	
PT	New growth factor related to vascular endothelial growth factor -	
PT	useful for inducing astroglial proliferation and promoting neuronal	
PT	survival	
PS	Example 3: Page 42-43; 113pp; English.	
CC	3 cDNA clones (T33611-13) code for splice variants (W00726-28)	
CC	of the human vascular endothelial growth factor-like polypeptide	
CC	SOM175 (see also W00725). They were identified in a human foetal	
CC	spleen library and respectively lack exon 6, exons 6-7, and exon 4	
CC	of the SOM175 gene (see also T33610). The cDNA clones can be	
CC	used to produce recombinant SOM175 proteins that are useful for	
CC	inducing astroglial proliferation and for promoting neural survival	
CC	and/or proliferation.	
SQ	Sequence 993 BP; 231 A; 307 C; 280 G; 175 T;	
Query Match	53.8%; Score 358; DB 23; Length 993;	
Best local similarity	99.7%; Pred. No. 2,83e-205;	
Matches 359; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Db	53 ccccccacagcccccctgctccacagcctgatacctgacccctggccacagagaaagtgtgtc 112	
Oy	48 ccccccacagcccccctgctccacagcctgatacctgacccctggccacagagaaagtgtgtc 107	
Db	113 atgataagatgtgtatactatcgcgctacccctgcagcccccggaggtgtgtgtcccttgac 172	
Oy	108 atgataagatgt 167	
Db	173 tgt 232	
Oy	168 tgt 227	
Db	233 ctgt 292	
Oy	228 ctgt 287	
Db	293 ccgagatgacatcctcattatcctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 352	
Oy	288 ccgagatgacatcctcattatcctggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 347	
Db	353 agaacaagcagcagtgatgt 412	
Oy	348 agaacaagcagcagtgatgt 407	
RESULT	9	
ID	T33613 standard; cDNA; 910 BP.	
AC	T33613;	
DT	30-NOV-1996 (first entry)	
DE	Vascular endothelial growth factor-like protein SOM175-e4 cDNA.	
KM	Vascular endothelial growth factor; VEGF; SOM175-e4; neuron;	
OS	Homo sapiens.	

	Key	Location/Qualifiers
FT	cds	3..308 /*tag= a
FT	signal_peptide	3..65 /*tag= b
FT	mat_peptide	66..305 /*tag= c
PN		
PD	W09627007-A1.	
PF	06-SEP-1996.	
PR	22-FEB-1996; AU0094.	
PR	02-MAR-1995; AU-001457.	
PR	20-NOV-1995; AU-006647.	
PR	22-DEC-1995; AU-007274.	
PI	(AMRA-) AMRAD OPERATIONS PTY LTD.	
PI	Grimmond S, Hayward NK, Larsson C, Nordenskjold M;	
PI	Weber G;	
DR	WPI: 96-412774/41.	
DR	P-PDSB: W00738.	
PT	New growth factor related to vascular endothelial growth factor -	
PT	useful for inducing astroglial proliferation and promoting neuronal	
PT	survival	
PS	Example 3: Page 47-48; 113pp; English.	
CC	3 CDNA clones (T33611-13) code for splice variants (W00726-28)	
CC	of the human vascular endothelial growth factor-like polypeptide	
CC	SOM175 (see also W00725).. They were identified in a human foetal	
CC	spleen library and respectively lack exon 6, exons 6+7, and exon 4	
CC	of the SOM175 gene (see also T33610). The cDNA clones can be	
CC	used to produce recombinant SOM175 proteins that are useful for	
CC	inducing astroglial proliferation and for promoting neural survival	
CC	and/or proliferation.	
SC	Sequence 910 BP; 182 A; 316 C; 254 G; 158 T;	
Query Match	43.2%; Score 288; DB 23; Length 910;	
Best Local Similarity	96.8%; Pred. No. 1,29e-160;	
Matches 303; Conservative	0; Mismatches 9; Indels 1; Gaps 1;	
Db	285 caccaagctccgcatgcagactataaaaaaggacagtgtcgtgtgaagccagacggcgatc 344	
Oy	354 CAGCGAGTGTAATGACGAGACTCTAAAAAAGGACAGTCGTGTGAAGCAACAAGGGCTGC 413	
Db	345 caccgcccaaacacagctcccacgccccgttctgttcgcggagcttggaacctgcgcccgagc 404	
Oy	414 TACTGCCACACCACGCTCCCAGCCCCCTTTCTGTTCCGCGGTGGACTCTCCCCGGAGC 473	
Db	405 accctccccaagtacatacaccca-tcccaactcagaagcccccctctcgtccacaagctg 463	
Oy	474 ACCCTCCCACTCATCAATCACCCAAATCCACTCAGGCCCAAGCCCTCTGCCACAGCTC 533	
Db	464 caccagacacacacagcgccttcgaccccccggaacctgcgctgcgcgtccagacgcgcag 533	
Oy	534 CACCAGACACCAACGATGCGCTTACCCCCCGAGACTGCGCTGCGGTGTGACAGCGCGAG 593	
Db	524 ctctctcgtttgccaaggcgagggttaagagctcaaccacgaacctgaagtgagcgagaa 583	
Oy	584 CTTCCTCCGTTGTAAGGGCGGGGCTTAGAGCTCAACCCAGACACCTGCAAGGTGGGAA 653	
Db	584 gctcggaaggtga 596	
Oy	654 GCTCGGAAGGTGA 666	
RESULT 10		
ID	T37910 standard; cDNA; 565 BP.	
AC	T37910;	
DT	28-APR-1997 (first entry)	
DE	Adult heart VEGF-B167 coding sequence.	
KM	Endothelial cell; proliferation; vascular endothelial growth factor; VRF	
KM	VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration;	
KM	vascular permeability factor; cell mitogen; angiogenesis; cell growth;	
KM	embryonic development; wound healing; tissue reorganisation; antihon-	
KM	cancer; metastatic risk; tumour cell; mouse; ss.	
OS	Mus musculus.	
NN	W09626736-A1.	

PD 06-SEP-1996: 002957.
PF 01-MAR-1996: US-397651.
PR 01-MAR-1995: US-397651.
PR 06-JUN-1995: US-469427.
PR 06-DEC-1995: US-569063.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Alltalo K, Eriksson U, Olofsson B, Pajusola K;
DR WPI: 96-412582/41.
PT Vascular endothelial growth factor VEGF-B proteins - useful to
PT accelerate angiogenesis in wound healing, also related nucleic acid
PT and antibodies for cancer diagnosis
PS Claim 1, Page 54-55; 107pp; English.
CC T37909-T37915 represent the coding sequences for the vascular endothelial
CC growth factor (VEGF) proteins of the invention, which promote endothelial
CC or mesodermal cell proliferation. VEGF is also a glycosylated cationic
CC dimer, and is sometimes referred to as vascular permeability factor
CC (VPF). VEGF has diverse effects, depending on the specific biological
CC context in which it is found. VEGF is a potent endothelial cell mitogen,
CC and directly contributes to induction of angiogenesis in vivo by
CC promoting endothelial cell growth during normal embryonic development,
CC wound healing, and tissue regeneration/reorganization. The VEGF proteins
CC of the invention share the angiogenic and other properties of VEGF, but
CC are distributed and expressed in tissues differently to VEGF. The
CC proteins can therefore be used to accelerate angiogenesis in wound
CC healing. Antibodies against the proteins can be used for inhibiting
CC angiogenesis. The antibodies can also be used diagnostically to
CC quantitatively detect VEGF-B. Primers complementary to the coding
CC sequences for the proteins of the invention can also be used to detect
CC VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy
CC specimens may be useful as an indicator of metastatic risk. VEGF-B
CC expression in a cell can be retarded using antisense sequences direct
CC against the VEGF coding sequences, this is especially useful in retarding
CC VEGF expression in tumour cells.
SQ Sequence 565 BP; 120 A; 179 C; 166 G; 100 T;

Query Match 42.8%; Score 285; DB 28; Length 565;
Best Local Similarity 90.1%; Pred. No. 1,056-158;
Matches 320; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

DB 54 cccaggccctgtgtcccaattgattgagccgcccaggaagaagtgtgcatgga 113
QY 53 CCCAGGCCCTGTCTCCACCCCTGATGCCCTGGCCACAGAGAAAGTGTCATGGA 112
DB 114 tagagctttatgcatggtccacatgcccagcagaggtgtgtgtccctcagcatg 173
QY 113 TAATGTGTATCTACCGCGCTACTCCAGCCCGGAGGTGTGTCCCTTGACTGTGG 172
DB 174 aactcatgagcaatgtgttcaacaactagttgccagctgtgtgactgtcagcgtgtg 233
QY 173 AGTCAATGGCAGCGTGGCCAAAGCTGTGTGCCACACTCGTAGCTGACGAGGCGTGTG 232
DB 234 gtgtgctgtccctgtgacatgagctgtgaaatgtgtccacttgggcaacacagtcgaa 293
QY 233 GTGGCTGCTCCCTGTGACGAGGCTGTGAGTGTGTGCCCACTGGCCACACCAAGTCCGGA 292
DB 294 tggagatcccatgcatcagctaccgagcagtgagctgtggggagagatgcccttgaagaac 353
QY 293 TGCAGATCCCTCATGATCGGTAACCGAGCTGAGCTGTGGGGAGATGTCCCTGGAAAGAC 352
DB 354 acagccaatgtgtaatgcagacccaataaagaagagatgtgtgtaagccagacag 408
QY 353 ACAGCCAGTGTGATGACGACCTAAAGGAGACAGTGTGTGAACCCAGACAG 407

RESULT 11
ID T13810 standard; CDNA: 1141 BP.
AC T13810:
DT 30-NOV-1996 (first entry)
DE Murine VRF167 CDNA
KW VRF: vascular endothelial growth factor: VEGF; SOM175; neuron;
KW astroglial proliferation; ss.

OS Mus musculus.
FH Key Location/Qualifiers
FT cds 166..732
FT /tag= a
FT signal_peptide 166..228
FT /tag= b
FT mat_peptide 229..729
FT /tag= c
FT repeat_region 1062..1065
FT /tag= d
FT /note= "polymorphic AC repeat region"
FT poly_a_signal 1085..1090
FT /tag= e

PN W09627007-A1.
PD 06-SEP-1996.
PF 22-FEB-1996; AU00924.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI (Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI: 96-412774/41.
DR P-PSDB: W00864.
PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Example 5; Fig 9; 113pp; English.
CC VRF169 CDNA (T13810) codes for a murine homologue (W00864) of an
CC alternatively spliced variant (W00726) of human vascular endothelial
CC growth factor-like polypeptide SOM175 (see also W00725), a protein
CC capable of inducing astroglial proliferation and of promoting neural
CC survival and/or proliferation. It was obtained from a new-born mouse
CC murine VRF gene library using SOM175 CDNA (see also T33610) as probe. The
CC murine VRF gene maps near to the centromere of chromosome 19. It is
CC highly expressed in embryo tissue and in the heart and brown fat of
CC adult mice. VRF169 lacks exon 6, found in VRF186 CDNA (T13809).
SQ Sequence 1141 BP; 256 A; 361 C; 313 G; 211 T;

Query Match 42.2%; Score 281; DB 23; Length 1141;
Best Local Similarity 89.6%; Pred. No. 3,656-156;
Matches 318; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

DB 221 cccaggccctgtgtcccaattgattgagccgcccaggaagaagtgtgcatgga 370
QY 53 CCCAGGCCCTGTCTCCACCCCTGATGCCCTGGCCACAGAGAAAGTGTCATGGA 112
DB 281 tagagctttatgcatggtccacatgcccagcagaggtgtgtgtccctcagcatg 340
QY 113 TAATGTGTATCTACCGCGCTACTCCAGCCCGGAGGTGTGTCCCTTGACTGTGG 172
DB 341 aactcatgagcaatgtgttcaacaactagttgccagctgtgtgactgtcagcgtgtg 400
QY 173 AGTCAATGGCAGCGTGGCCAAAGCTGTGTGCCACACTCGTAGCTGACGAGGCGTGTG 232
DB 401 gtgtgctgtccctgtgacatgagctgtgaaatgtgtccacttgggcaacacagtcgaa 460
QY 233 GTGGCTGCTCCCTGTGACGAGGCTGTGAGTGTGTGCCCACTGGCCACACCAAGTCCGGA 292
DB 461 tggagatcccatgcatcagctaccgagcagtgagctgtggggagagatgcccttgaagaac 520
QY 293 TGCAGATCCCTCATGATCGGTAACCGAGCTGAGCTGTGGGGAGATGTCCCTGGAAAGAC 352
DB 521 acagccaatgtgtaatgcagacccaataaagaagagatgtgtgtaagccagacag 575
QY 353 ACAGCCAGTGTGATGACGACCTAAAGGAGACAGTGTGTGAACCCAGACAG 407

RESULT 12
ID T37912 standard; CDNA: 405 BP.
AC T37912:
DT 28-APR-1997 (first entry)
DE VEGF-B112 coding sequence.

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Db	191	acaccaagtcggaatgcagatccctcatgattccagttaccgagcagtagcttggtgggagat	250
Qy	279	GCACCAAAATCCGGATCGCATCTCATGATCCGGTACCOCGAGCATGAGTGGGGGAGAT	338
Db	251	gtcccttggaagaaacacagccaatgtgtaatgcagaccaaataaaagagagatgctgtg	310
Qy	339	GTCCTGGAAACACACACCAGTGTGATGCAGACGACTTAAAAAAA--GGACAGTGTGTG	396
Db	311	aagcacgacag	321
Qy	397	AAGCAGACAG	407

RESULT	14	
ID	T37911	standard; cDNA; 591 BP.
AC	T37911	
DT	28-APR-1997	(first entry)
DE	Adult heart VEGF-B174 coding sequence.	
KW	Endothelial cell; proliferation; vascular endothelial growth factor; VEGF;	
KW	VEGF; endothelial cell; proliferation; mesodermal cell; cationic dimer; tissue regeneration;	
KW	vascular permeability factor; cell mitogen; angiogenesis; cell growth;	
KW	embryonic development; wound healing; tissue reorganisation; antibody;	
KW	cancer; metastatic risk; tumour cell; mouse; ss.	
OS	Mus musculus.	
PN	MO9626736-A1.	
PD	06-SEP-1996.	
PF	01-MAR-1996; U02957.	
PR	01-MAR-1995; US-397651.	
PR	06-JUN-1995; US-469427.	
PR	06-DEC-1995; US-569063.	
PA	(LUDW-) LUDWIG INST CANCER RES.	
PT	(UYHE-) UNIV HELSINKI LICENSING LTD OY.	
PI	Altalo K, Eriksson U, Olofsson B, Pajusola K;	
DR	WPI: 96-412582/41.	
DR	P-PDSB: W04827.	
PT	Vascular endothelial growth factor VEGF-B proteins - useful to	
PT	accelerate angiogenesis in wound healing, also related nucleic acid	
PR	and antibodies for cancer diagnosis	
PS	Claim 1: Page 56: 107pp: English.	
CC	T37909-T37915 represent the coding sequences for the vascular endothelial	
CC	growth factor (VEGF) proteins of the invention, which promote endothelial	
CC	or mesodermal cell proliferation. VEGF is also a glycosylated cationic	
CC	dimer, and is sometimes referred to as vascular permeability factor	
CC	(VPF). VEGF has diverse effects, depending on the specific biological	
CC	context in which it is found. VEGF is a potent endothelial cell mitogen,	
CC	and directly contributes to induction of angiogenesis in vivo by	
CC	promoting endothelial cell growth during normal embryonic development,	
CC	wound healing, and tissue regeneration/reorganisation. The VEGF proteins	
CC	of the invention share the angiogenic and other properties of VEGF, but	
CC	are distributed and expressed in tissues differently to VEGF. The	
CC	proteins can therefore be used to accelerate angiogenesis in wound	
CC	healing. Antibodies against the proteins can be used for inhibiting	
CC	angiogenesis. The antibodies can also be used diagnostically to	
CC	quantitatively detect VEGF-B. Primers complementary to the coding	
CC	sequences for the proteins of the invention can also be used to detect	
CC	VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy	
CC	specimens may be useful as an indicator of metastatic risk. VEGF-B	
CC	expression in a cell can be retarded using antisense sequences direct	
CC	against the VEGF coding sequences, this is especially useful in retarding	
CC	VEGF expression in tumour cells.	
SO	Sequence 591 BP; 126 A; 186 C; 174 G; 105 T;	

Query Match	27.5%	Score 183;	DB 28;	Length 591;
Best Local Similarity	87.38;	Pred. No. 2.78e-94;		
Matches	214;	Conservative	0;	Mismatches 31;
				Indels 0;
				Gaps 0;

Db 59 ccagagccccctgtagcccaattatagccccagccacacagaaagatgtgccatga 118
Qy 53 cccagagccccctgtctcccaactatagcccttgccccacacagagaaagtgctatgga 112

Dd 119 tagagcttattatgcacgtgccacatgccaagccagagagtggtgtgctctcagcatg 178
Qy 113 tagagtgataactgcgccttactgcgcagccccagagagtggtgtcccttgactctgg 172

Db	179	aaccataggsgaatgtgtgcaacaactagtgtcccaagtctgtgactgtgcaacgcctgtg	238
Qy	173	AGCTCATGGGGCACCGTGGGCCCAAAAGTGGTGCCACACTCGTAGCTGCACACGCTG	232
Db	239	gttgctctgtgcctggaagatggcctgtgaatgtgtgcccactgtggcaacaccaagtccga	298
Qy	233	GTGGCTGTGTGCCCTGGACGATGGCCCTGTGAGTGTGTGCCACTGTGGGACACACCAAGTCGGA	292
Db	299	tgacag 303	
Qy	293	TGCAG 297	

RESULT	15
ID	Q11099 standard; DNA; 366 BP.
AC	Q11099;
DT	08-MAY-1991 (first entry)
DE	Human vascular endothelial cell growth factor 121.
KW	Bovine vascular endothelial cell growth factor; angiogenesis; wound healing; hVEGF; PDGF; ss.
OS	Bos taurus.
PH	Key
FT	Location/Qualifiers
FT	1..363
FT	/*tag= a
FT	/product= VEGF
PN	M09102058-A.
PD	21-FEB-1991.
PR	27-JUL-1990; U04227.
PR	27-JUL-1989; US-387545.
PR	14-DEC-1989; US-450883.
PA	(CALB-). CALIF BIOTECHN INC.
PI	Tischer ER, Abraham, Fiddes JC, Mitchell RL;
DR	Wpi: 91-073534/10.
DR	P-PSDS: R11386.
FT	DNA encoding vascular endothelial cell growth factor - used for
PT	producing the factor for angiogenesis and re-endothelialisation
PT	in wound healing
PS	Disclosure: Fig 7(1-2); 94pp; English.
CC	Fetal human vascular smooth muscle cells mRNA was isolated
CC	for the preparation of a cDNA library.
CC	The two forms of VEGF (Q10797 and Q10917) which arise through
CC	different message splicing, have different properties. In partic.
CC	hVEGF121 does not bind to heparin leaving more of the protein free to
CC	bind to VEGF receptor and increase the half-life and distribution of
CC	the protein in circulation, whereas hBEGF165 binds heparin strongly.
CC	The product can be used for angiogenesis and re-endothelialisation
CC	of inner vascular surfaces in wound healing, e.g. treatment of full-
CC	thickness wounds such as dermal ulcers, venous ulcers and diabetic
CC	ulcers, burns, in surgery, in balloon angioplasty and for the in
CC	vitro culturing of endothelial cells. Hybrid growth factors of PDGF
CC	and VEGF can exhibit a mitogenic profile between each factor and
CC	e.g. preventing the growth of tumours.
CC	VEGF analogues in which CTS residues are subst. are more stable.
CC	See also Q10791-93; Q10796-97; Q10806-08 and Q11099.
SO	Sequence 366 BP; 110 A; 89 C; 103 G; 64 T;

Query Match	7.2%;	Score 48;	DB 2;	Length 366;
Best Local Similarity	68.0%;	Pred. No. 7.17e-13;		
Matches 119;	Conservative 0;	Mismatches 53;	Indels 3;	Gaps 3

Db 150 ctgtgtgacctatgtcgatgcggagagctcgtgaaagacgaagagcctgtgagtgtgac 209

Qy 210 ctgcctgactgtgcagccgctctgtgtgctgctgccctgcacatgacctgtgagtgtgcc 265

Db 210 cactgtgagatccacatccatcagatgatagtcgatgataaaccttaccagaagcagca 265

Qy 270 cactgtggcagcaccagctccgaaatgcagatcttatatccgga-c-cggag-cagtca 325

Db 270 catagagagatgtgactctctacacagcaacaatgtgaaatgcagaccaaagaagaa 324

Qy 327 gctgtggcgaagtgtcctctggaagaacacagccactgtgaaatgcagaccttataaaaa 381

Tue Dec 1 13:40:19 1998

US-09-033-662-1.rng

Page 10

Search completed: Tue Dec 1 12:26:11 1998
job time : 214 secs.

 WISE (TM)

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MPsrch_un n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 1 10:39:03 1998; MasPar time 990.87 Seconds

Tabular output not generated. 1481.258 Million cell updates/sec

Title: >US-09-033-662-1
 Description: (1-666) from US09033662.seq
 Perfect Score: 666
 N.A. Sequence: 1 ATGAGAGCTGTAGATAAG.....GCCGAGCTGCGAAGTGA 666
 Comp: TACCTTCACATCTTATTC.....CGCCTTCGACGCTTCACCT

Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 567134 segs, 1101898692 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

emb155
 1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
 13:em_ro 14:em_v1
 genbank107

Database:
 15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov
 21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pl1
 26:gb_pl2 27:gb_pl3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy
 32:gb_un 33:gb_v1

Statistics: Mean 10.510; Variance 5.631; scale 1.866

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	604	90.7	1079	25	HSU43368 Human VEGF related fac	0.00e+00
2	602	90.4	759	27	HSU52819 Human VEGF related fac	0.00e+00
3	483	72.5	1336	28	MMU52830 Mus musculus vascular	0.00e+00
4	483	72.5	1336	28	MMU52835 Mus musculus VEGF-rela	0.00e+00
5	360	54.1	567	25	HSU43369 Human VEGF related fac	1.99e-250
6	360	54.1	570	21	HSU43369 Human VEGF related fac	1.99e-250
7	360	54.1	570	25	HSU48801 Human vascular endothel	1.99e-250
8	285	42.8	567	28	MMU43837 Mus musculus VEGF-rela	1.61e-191
9	285	42.8	795	28	MMU48800 Mus musculus vascular	1.61e-191
10	285	42.8	795	28	AF022925 Rattus norvegicus vasc	2.17e-188
11	281	42.2	349	28	AF022925 Rattus norvegicus vasc	2.47e-174
12	263	39.5	405	21	AF022925 Rattus norvegicus vasc	1.19e-162
13	248	37.2	453	28	AF022952 Rattus norvegicus vasc	1.19e-162

14	241	36.2	886	21	136625	Sequence 1 from patent	3.31e-157
15	183	27.5	591	21	136627	Sequence 6 from patent	2.06e-112
16	67	10.1	7218	21	166494	Sequence 14 from patent	1.83e-15
17	56	8.4	226	19	AF022179	Oryctolagus cuniculus	5.55e-15
18	50	7.5	576	25	S82167	simVEGF165-vascular en	5.04e-15
19	48	7.2	576	21	A64392	Sequence 5 from patent	9.95e-11
20	48	7.2	630	27	HS401038	Human VEGF related fac	9.95e-11
21	48	7.2	649	25	HSVEGF	H.sapiens vegf gene 10	9.95e-11
22	48	7.2	774	21	E13332	cDNA encoding vascular	9.95e-11
23	48	7.2	774	21	E13315	Human mRNA for vascu	9.95e-11
24	48	7.2	774	10	E11017	A part of psu 2 includ	9.95e-11
25	48	7.2	815	27	S85192	Human VEGF related fac	9.95e-11
26	48	7.2	990	25	HUVEGF	Human heparin-binding	9.95e-11
27	48	7.2	1195	25	HUVEGF	Human vascular permeab	9.95e-11
28	48	7.2	1649	21	A64396	Sequence 9 from patent	9.95e-11
29	48	7.2	1664	21	A64404	Sequence 17 from patent	9.95e-11
30	48	7.2	1787	21	A64394	Sequence 7 from patent	9.95e-11
31	48	7.2	1790	21	A64400	Sequence 13 from patent	9.95e-11
32	48	7.2	1790	21	A64398	Sequence 11 from patent	9.95e-11
33	48	7.2	1832	21	A64402	Sequence 15 from patent	9.95e-11
34	46	6.9	3166	27	AF022375	Human VEGF related fac	1.90e-12
35	44	6.6	573	25	HUVEGF3	Human vascular endoth	3.52e-11
36	44	6.6	573	19	SVVEGF	S. scrofa mRNA for vasc	3.52e-11
37	42	6.3	311	26	HUVDID10M3	Human HepG2 3' region	6.28e-10
38	42	6.3	495	28	GPVEGF	Guinea pig vascular en	6.28e-10
39	42	6.3	802	19	BOVEGF	Bovine vascular endoth	6.28e-10
40	42	6.3	934	19	BOVEGF	Bovine vascular endoth	6.28e-10
41	42	6.3	1536	19	BOVEGF	Bovine heparin-binding	6.28e-10
42	42	6.3	5025	25	HUVRGM	Human 28S ribosomal RN	6.28e-10
43	42	6.3	4299	25	HSU13369	Human ribosomal DNA co	6.28e-10
44	41	6.2	7218	21	166494	Sequence 14 from paten	2.61e-07
45	40	6.0	457	28	S38100	vascular endothelial g	1.07e-08

ALIGNMENTS

RESULT LOCUS	1	HSU43368	1079 bp	mRNA	PRI	07-MAR-1996
DEFINITION	1	Human VEGF related factor isoform VRF166 precursor (VRF) mRNA,				
ACCESSION		U43368				
KEYWORDS		g1216395				
SOURCE		human.				
ORGANISM		human.				
REFERENCE		Grimmond, S., Lagercrantz, J., Drinkwater, C., Sillins, G., Townsend, S., Vertebriate, Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS		Pollock, P., Gotley, D., Carson, E., Rakar, S., Nordenskjold, M., Ward, L., Hayward, N. and Weber, G.				
TITLE		Cloning and characterization of a novel human gene related to				
JOURNAL		vascular endothelial growth factor				
AUTHORS		Genome Res. 6 (2), 122-129 (1996)				
TITLE		Sillins, G. U.				
JOURNAL		Submitted (15-DEC-1995) Ginters U. Sillins, Human Genetics,				
FEATURES		Queensland Institute of Medical Research, Herston, Queensland,				
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NID 91488258
KEYWORDS
SOURCE human
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Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 755)
REFERENCE
AUTHORS Olofsson,B., Pajusola,K., Kaipainen,A., von Euler,G., Joukov,V.,
Saksela,O., Orpana,A., Pettersson,R.F., Alltalo,K. and Eriksson,B.
Vascular endothelial growth factor B, a novel growth factor for
endothelial cells
Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2576-2581 (1996)
JOURNAL MEDLINE
REFERENCE
AUTHORS Olofsson,B., Pajusola,K., von Euler,G., Chillov,D., Alltalo,K. and
Eriksson,B.
Genomic organization of the mouse and human genes for vascular
endothelial growth factor B (VEGF-B) and characterization of a
second splice isoform
J. Biol. Chem. 271 (32), 19310-19317 (1996)
3 (bases 1 to 755)
REFERENCE
AUTHORS Eriksson,B., Alltalo,K., Olofsson,B. and Pajusola,K.
Direct Submission
Submitted (27-MAR-1996) Ulf Eriksson, Ludwig Institute for Cancer
Research, Karolinska Institutet, Doktorringen 12A, Stockholm S-171,
77, Sweden
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RESULT 2
LOCUS HSU52819 755 bp mRNA PRI 08-OCT-1996
DEFINITION Human vascular endothelial growth factor B 186 (VEGF-B) precursor,
ACCESSION U52819

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BEST AVAILABLE COPY

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RESULT 3
LOCUS MM052820 896 bp mRNA ROD 08-OCT-1996
DEFINITION Mus musculus vascular endothelial growth factor B 186 (VEGF-B)
ACCESSION U52820
NID 91488260
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; Euthera; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 896)
AUTHORS Olofsson,B., Pajusola,K., Kaipainen,A., von Euler,G., Joukov,V.,
Saksela,O., Orpana,A., Petersson,R.F., Allitalo,K. and Eriksson,U.
Vascular endothelial growth factor B, a novel growth factor for
endothelial cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2576-2581 (1996)
MEDLINE 96197355
REFERENCE 2 (bases 1 to 896)
AUTHORS Olofsson,B., Pajusola,K., von Euler,G., Chliov,D., Allitalo,K. and
Eriksson,U.
Genomic organization of the mouse and human genes for vascular
endothelial growth factor B (VEGF-B) and characterization of a
second splice isoform
J. Biol. Chem. 271 (32), 19310-19317 (1996)
TITLE
JOURNAL
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AUTHORS
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JOURNAL
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AUTHORS
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LOCUS MM043836 1236 bp mRNA ROD 04-DEC-1996
DEFINITION Mus musculus VEGF-related factor mvr186 precursor mRNA, complete
cds.
ACCESSION U43836
NID 91703460
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1236)
AUTHORS Townsend,S., Lagercrantz,J., Grimmond,S., Sillis,G.,
Nordenskjold,M., Weber,G. and Hayward,N.
Characterization of the murine VEGF-related factor gene
J. Biochem. Biophys. Res. Commun. 220 (3), 922-928 (1996)
MEDLINE 96183052
REFERENCE 2 (bases 1 to 1236)
AUTHORS Hayward,N.K.

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TITLE Direct Submission
JOURNAL Submitted (21-DEC-1995) Nicholas K. Hayward, Joint Experimental
Oncology Unit, Queensland Institute of Medical Research, Bancroft
Centre, 300 Herston Rd, Herston, Brisbane, Queensland, 4029,
Australia
COMMENT On Dec 4, 1996 this sequence version replaced gi:1314333.
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Matches 551; Conservative 0; Mismatches 62; Indels 1; Gaps 1;
Db 248 CCCAGGCCCTGTGTCCAGTTTGTATGGCCCGCCAGACAGAAAGTGTGCCATGA 307
QY 53 CCCAGGCCCTGTGTCCAGTTTGTATGGCCCGCCAGACAGAAAGTGTGCCATGA 112
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QY 653 AGCTGCGAAGTGA 666
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DEFINITION Human VEGF related factor isoform VRF167 precursor (VRF) mRNA.
ACCESSION U43369
NID 91216397
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL. Direct Submission
REFERENCE Silins, G.U.
TITLE Submitted (15-DEC-1995) Ginters U. Silins, Human Genetics,
Queensland Institute of Medical Research, Herston, Queensland,
4029, Australia
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RESULT 8
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DEFINITION Sequence 4 from patent US 5607918.
ACCESSION 136626
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REFERENCE
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  Unclassified.
AUTHORS
  Eriksson, U., Olofsson, B., Allitalo, K. and Pajusola, K.
TITLE
  Vascular endothelial growth factor-B and DNA coding therefor
JOURNAL
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DEFINITION Mus musculus VEGF-related factor mvrfl67 precursor mRNA, complete
  cds.
ACCESSION U43837
NID 91314335
KEYWORDS
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  house mouse.
ORGANISM
  Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
  Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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REFERENCE
  1 (bases 1 to 567)
  Townsend, S., Lagercrantz, J., Grimmond, S., Sillins, G.,
  Nordenskjold, M., Weber, G. and Hayward, N.
  Characterization of the murine VEGF-related factor gene
  Biochem. Biophys. Res. Commun. 220 (3), 922-928 (1996)
JOURNAL
  96183052
MEDLINE
  2 (bases 1 to 567)
  Hayward, N.K.
  Direct Submission
  Submitted (21-DEC-1995) Nicholas K. Hayward, Joint Experimental
  Oncology Unit, Queensland Institute of Medical Research, Bancroft
  Centre, 300 Herston Rd, Herston, Brisbane, Queensland, 4029,

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RESULT 10
LOCUS MMU48800 795 bp mRNA ROD 19-AUG-1996
DEFINITION Mus musculus vascular endothelial growth factor B precursor
  (VEGF-B) mRNA, complete cds.
ACCESSION U48800
NID 91234824
KEYWORDS
  house mouse.
SOURCE
  house mouse.
ORGANISM
  Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
  Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
  Murinae; Mus.
REFERENCE
  1 (bases 1 to 795)
  Olofsson, B., Pajusola, K., Kaipainen, A., von Euler, G., Joukov, V.,
  Saksela, O., Orpana, A., Petersson, R.F., Allitalo, K. and Eriksson, U.
  Vascular endothelial growth factor B, a novel growth factor for
  endothelial cells
  Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2576-2581 (1996)
JOURNAL
  96197355
MEDLINE

```

Kodentia; Sciurognathi; Muridae; Murinae; Rattus.

1. 1400
SOURCE
/organism="unknown"

ORIGIN

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 Best Local Similarity 89.7%; Pred. No. 2,47e-174;
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 QY 173 AGCTCATGGGCACTGTGTGCAACAGCTGTGTGCAACAGCTGTGTGCAACAGCTGTGTG 232
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 Db 299 TGCAGATCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 358
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 QY 293 TGCAGATCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 352
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 Db 359 ACAGCCAAATGTGAATGACAGCAACCAAAAAA 389
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 QY 353 ACAGCCAAATGTGAATGACAGCAACCAAAAAA 383
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RESULT 13

LOCUS AF022952 453 bp mRNA
 DEFINITION Rattus norvegicus vascular endothelial growth factor B mRNA,
 partial cds.
 ACCESSION AF022952
 NID 92766601

KEYWORDS

SOURCE

ORGANISM

REFERENCE

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BEST AVAILABLE COPY

RESULT 15
LOCUS 136627 591 bp DNA PAT 13-MAR-1997
DEFINITION Sequence 6 from patent US 5607918.
ACCESSION 136627
NID 92086452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 591)
AUTHORS Eriksson,U., Olofsson,B., Allitalo,K. and Pajusola,K.
TITLE Vascular endothelial growth factor-B and DNA coding therefor
JOURNAL Patent: US 5607918-A 6 04-MAR-1997;
FEATURES
source 1..591
location/Qualifiers
BASE COUNT 126 a 186 c 174 g 105 t
ORIGIN
Query Match 27.5%; Score 183; DB 21; Length 591;
Best Local Similarity 87.3%; Pred. No. 2,06e-112;
Matches 214; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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QY 113 TAGATGTGTATCTCGCGCTAAGCTGCAAGCCCGGAGGTGTGTGCTGTGCTGTGG 172
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